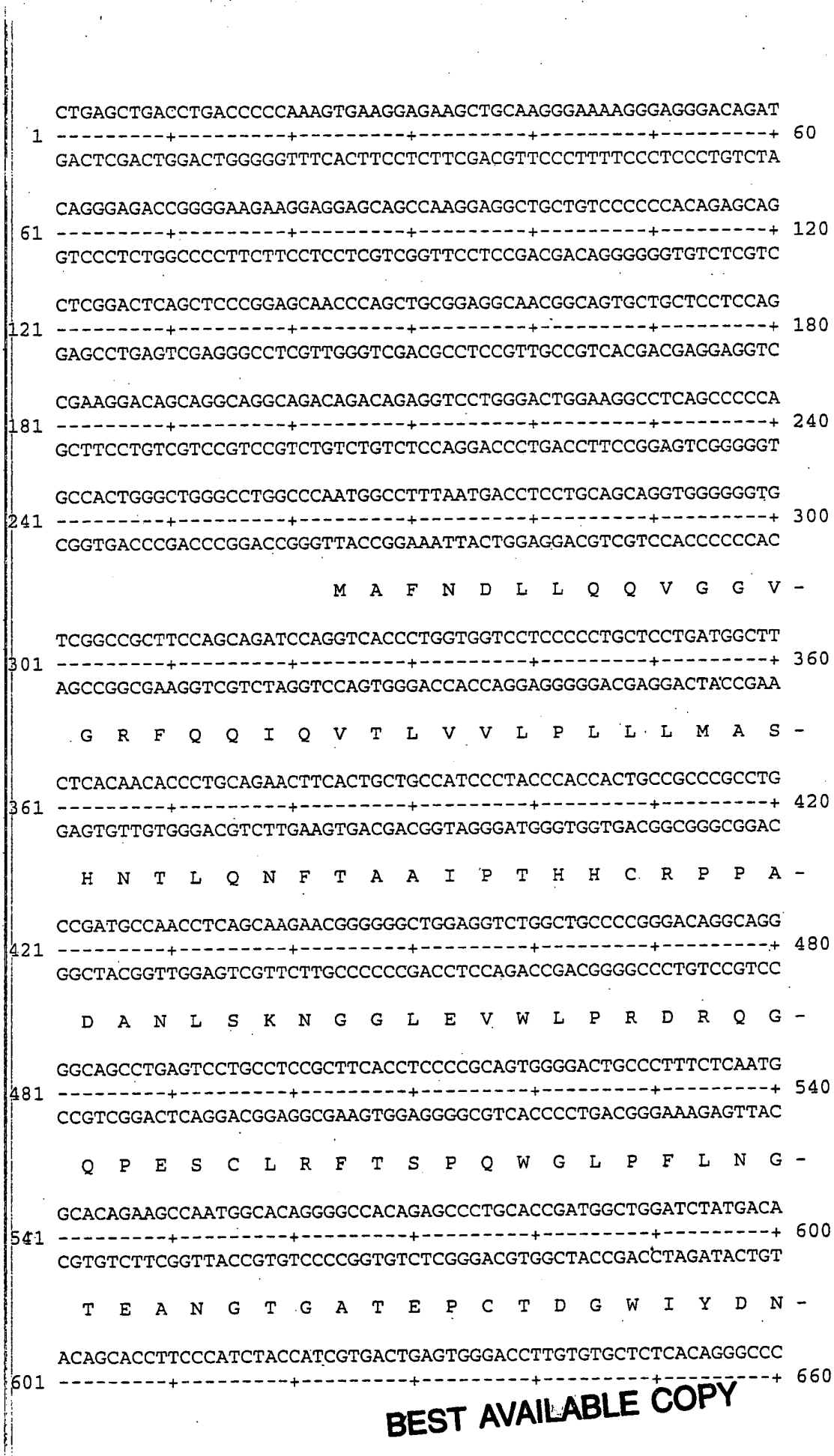


FIGURE 1
Sheet 1 of 4

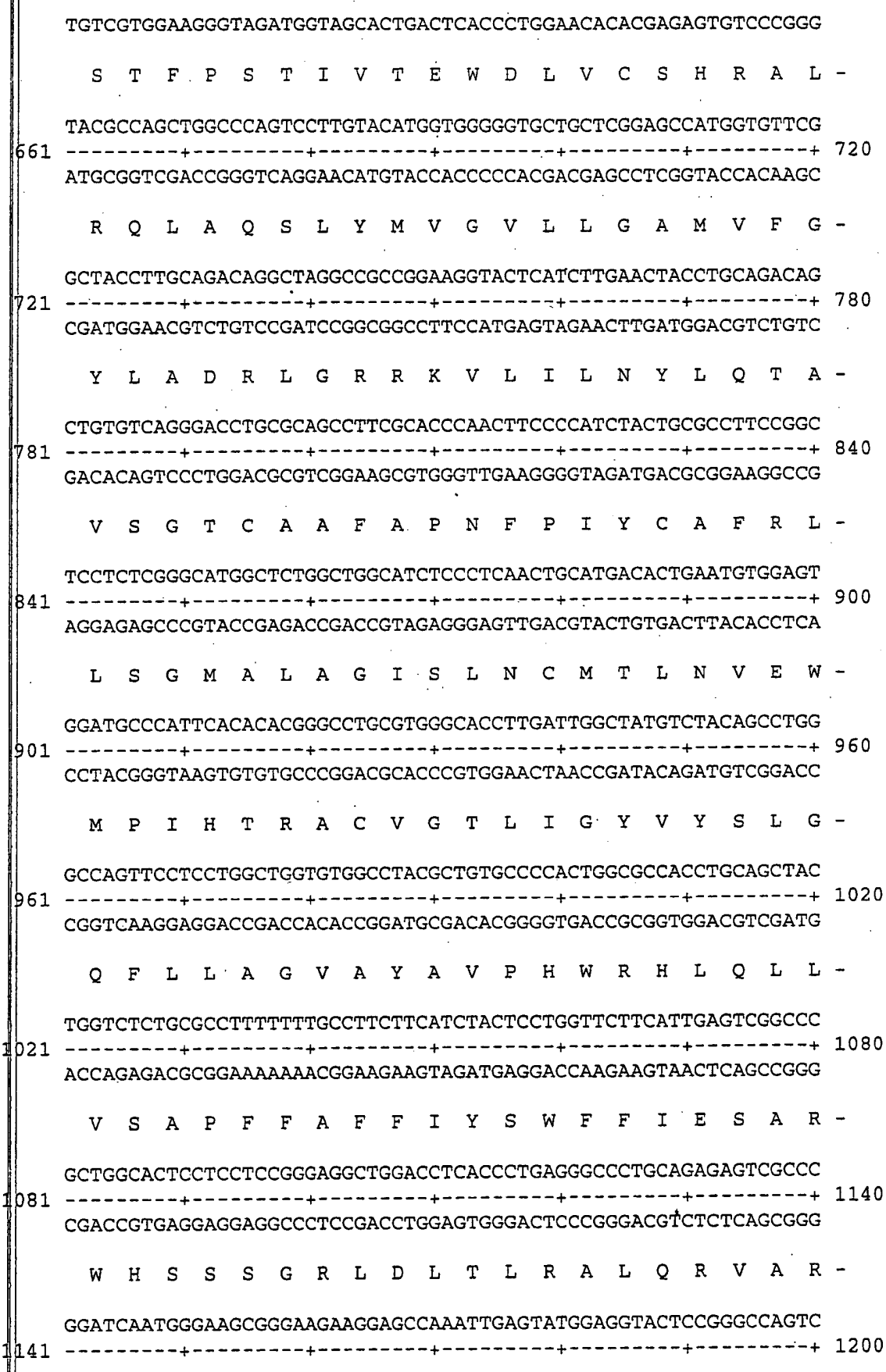


FIGURE 1
Sheet 2 of 4

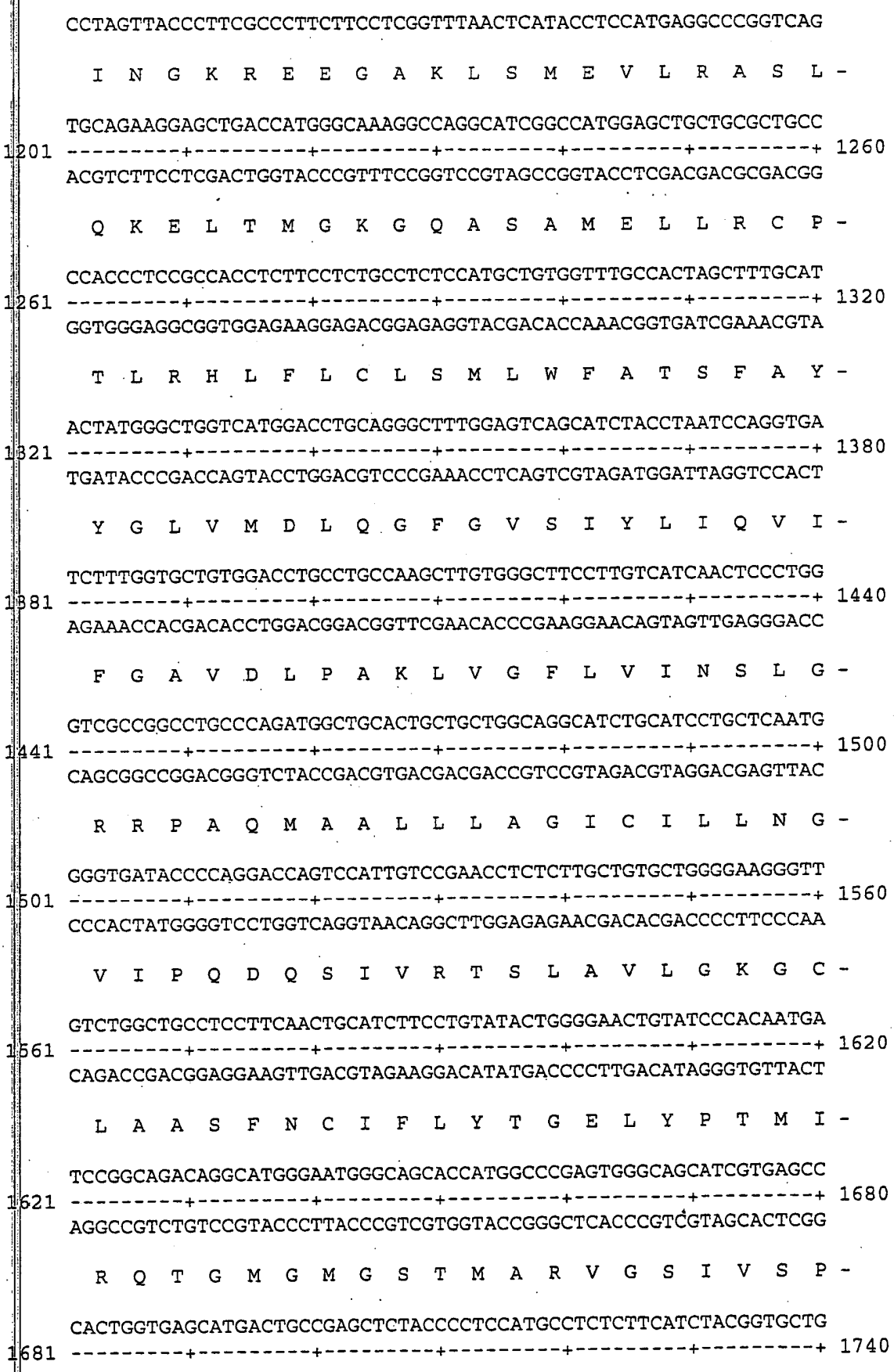


FIGURE 1
Sheet 3 of 4

```
GTGACCACTCGTACTGACGGCTCGAGATGGGGAGGTACGGAGAGAAGTAGATGCCACGAC

  L  V  S  M  T  A  E  L  Y  P  S  M  P  L  F  I  Y  G  A  V -

TTCCTGTGGCCGCCAGCGCTGTCACTGTCCTCCTGCCAGAGACCCTGGGCCAGCCACTGC
1741 ---------+---------+---------+---------+---------+---------+ 1800
AAGGACACCGGCGGTCGCGACAGTGACAGGAGGACGGTCTCTGGGACCCGGTCGGTGACG

  P  V  A  A  S  A  V  T  V  L  L  P  E  T  L  G  Q  P  L  P -

CAGACACGGTGCAGGACCTGGAGAGCAGGAAAGGGAAACAGACGCGACAGCAACAAGAGC
1801 ---------+---------+---------+---------+---------+---------+ 1860
GTCTGTGCCACGTCCTGGACCTCTCGTCCTTTCCCTTTGTCTGCGCTGTCGTTGTTCTCG

  D  T  V  Q  D  L  E  S  R  K  G  K  Q  T  R  Q  Q  Q  E  H -

ACCAGAAGTATATGGTCCCACTGCAGGCCTCAGCACAAGAGAAGAATGGACTCTGAGGAC
1861 ---------+---------+---------+---------+---------+---------+ 1920
TGGTCTTCATATACCAGGGTGACGTCCGGAGTCGTGTTCTCTTCTTACCTGAGACTCCTG

  Q  K  Y  M  V  P  L  Q  A  S  A  Q  E  K  N  G  L  *

TGAGAAGGGGCCTTACAGAACCCTAAAGGGAGGGAAGGTCCTACAGGTCTCCGGCCACCC
1921 ---------+---------+---------+---------+---------+---------+ 1980
ACTCTTCCCCGGAATGTCTTGGGATTTCCCTCCCTTCCAGGATGTCCAGAGGCCGGTGGG

ACACAAGGAGGAGGAAGAGGAAATGGTGACCCAAGTGTGGGGGTTGTGGTTCAGGAAAGC
1981 ---------+---------+---------+---------+---------+---------+ 2040
TGTGTTCCTCCTCCTTCTCCTTTACCACTGGGTTCACACCCCCAACACCAAGTCCTTTCG

ATCTTCCCAGGGGTCCACCTCCCTTTATAAACCCCACCAGAACCACATCATTAAAAGGTT
2041 ---------+---------+---------+---------+---------+---------+ 2100
TAGAAGGGTCCCCAGGTGGAGGGAAATATTTGGGGTGGTCTTGGTGTAGTAATTTTCCAA

TGACTGCGCACCAAAAAAAAAAAAAAA
2101 ---------+---------+------- 2127
ACTGACGCGTGGTTTTTTTTTTTTTT
```

FIGURE 1
Sheet 4 of 4

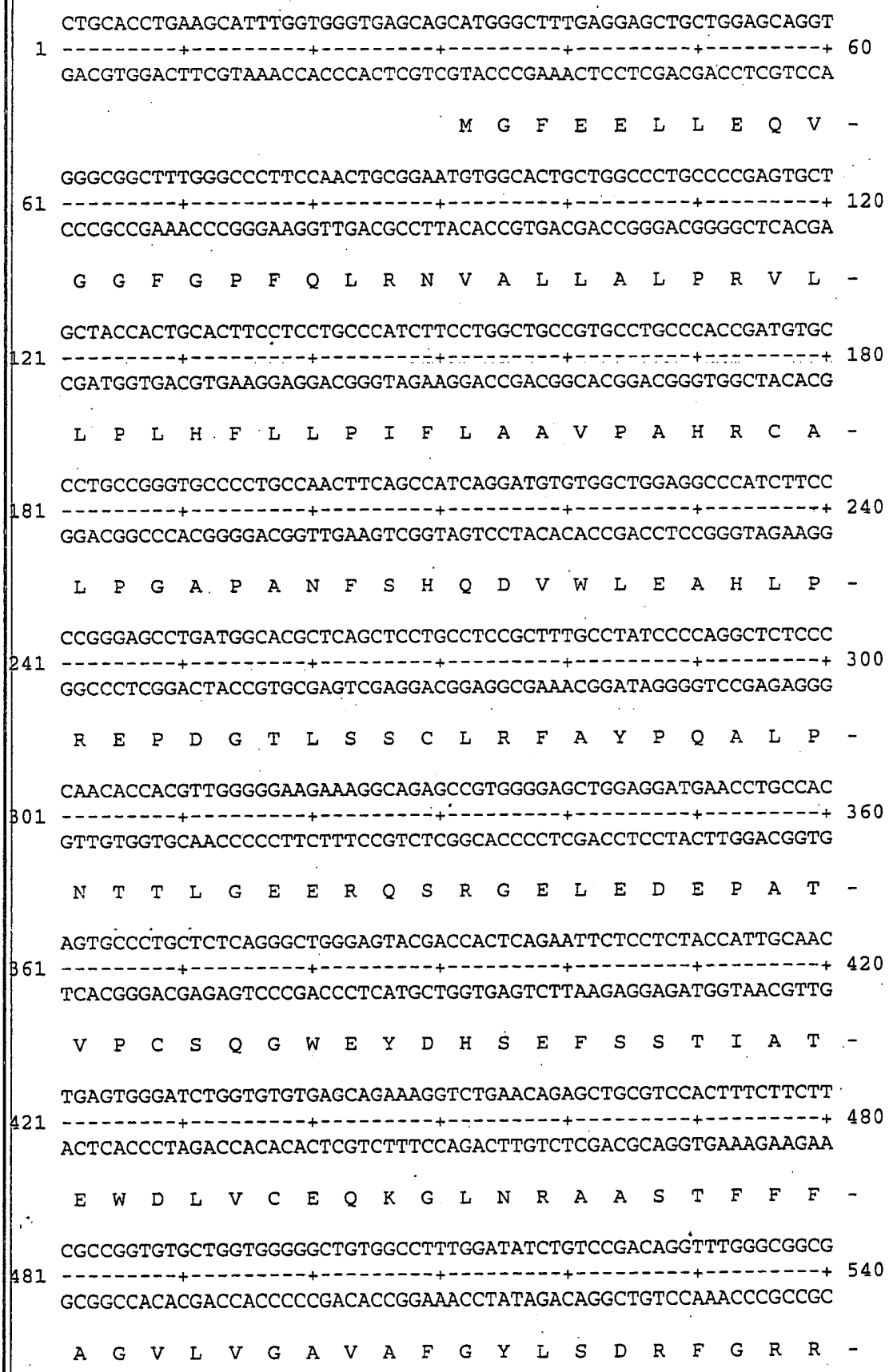

CTGCACCTGAAGCATTTGGTGGGTGAGCAGCATGGGCTTTGAGGAGCTGCTGGAGCAGGT
1 60
GACGTGGACTTCGTAAACCACCCACTCGTCGTACCCGAAACTCCTCGACGACCTCGTCCA
M G F E E L L E Q V -
GGGCGGCTTTGGGCCCTTCCAACTGCGGAATGTGGCACTGCTGGCCCTGCCCCGAGTGCT
61 120
CCCGCCGAAACCCGGGAAGGTTGACGCCTTACACCGTGACGACCGGGACGGGGCTCACGA
G G F G P F Q L R N V A L L A L P R V L -
GCTACCACTGCACTTCCTCCTGCCCATCTTCCTGGCTGCCGTGCCTGCCCACCGATGTGC
121 180
CGATGGTGACGTGAAGGAGGACGGGTAGAAGGACCGACGGCACGGACGGGTGGCTACACG
L P L H F L L P I F L A A V P A H R C A -
CCTGCCGGGTGCCCCTGCCAACTTCAGCCATCAGGATGTGTGGCTGGAGGCCCATCTTCC
181 240
GGACGGCCCACGGGGACGGTTGAAGTCGGTAGTCCTACACACCGACCTCCGGGTAGAAGG
L P G A P A N F S H Q D V W L E A H L P -
CCGGGAGCCTGATGGCACGCTCAGCTCCTGCCTCCGCTTTGCCTATCCCCAGGCTCTCCC
241 300
GGCCCTCGGACTACCGTGCGAGTCGAGGACGGAGGCGAAACGGATAGGGGTCCGAGAGGG
R E P D G T L S S C L R F A Y P Q A L P -
CAACACCACGTTGGGGGAAGAAAGGCAGAGCCGTGGGGAGCTGGAGGATGAACCTGCCAC
301 360
GTTGTGGTGCAACCCCCTTCTTTCCGTCTCGGCACCCCTCGACCTCCTACTTGGACGGTG
N T T L G E E R Q S R G E L E D E P A T -
AGTGCCCTGCTCTCAGGGCTGGGAGTACGACCACTCAGAATTCTCCTCTACCATTGCAAC
361 420
TCACGGGACGAGAGTCCCGACCCTCATGCTGGTGAGTCTTAAGAGGAGATGGTAACGTTG
V P C S Q G W E Y D H S E F S S T I A T -
TGAGTGGGATCTGGTGTGTGAGCAGAAAGGTCTGAACAGAGCTGCGTCCACTTTCTTCTT
421 480
ACTCACCCTAGACCACACACTCGTCTTTCCAGACTTGTCTCGACGCAGGTGAAAGAAGAA
E W D L V C E Q K G L N R A A S T F F F -
CGCCGGTGTGCTGGTGGGGGCTGTGGCCTTTGGATATCTGTCCGACAGGTTTGGGCGGCG
481 540
GCGGCCACACGACCACCCCCGACACCGGAAACCTATAGACAGGCTGTCCAAACCCGCCGC
A G V L V G A V A F G Y L S D R F G R R -

FIGURE 2

```
   GCGTCTGCTGCTGGTAGCCTACGTGAGTACCCTGGTGCTGGGCCTGGCATCTGCAGCCTC
541 ---------+---------+---------+---------+---------+---------+ 600
   CGCAGACGACGACCATCGGATGCACTCATGGGACCACGACCCGGACCGTAGACGTCGGAG

    R  L  L  L  V  A  Y  V  S  T  L  V  L  G  L  A  S  A  A  S  -

   CGTCAGCTATGTAATGTTTGCCATCACCCGCACCCTTACTGGCTCAGCCCTGGCTGGTTT
601 ---------+---------+---------+---------+---------+---------+ 660
   GCAGTCGATACATTACAAACGGTAGTGGGCGTGGGAATGACCGAGTCGGGACCGACCAAA

    V  S  Y  V  M  F  A  I  T  R  T  L  T  G  S  A  L  A  G  F  -

   TACCATCATCGTGATGCCACTGGAGCTGGAGTGGCTGGATGTGGAGCACCGCACCGTGGC
661 ---------+---------+---------+---------+---------+---------+ 720
   ATGGTAGTAGCACTACGGTGACCTCGACCTCACCGACCTACACCTCGTGGCGTGGCACCG

    T  I  I  V  M  P  L  E  L  E  W  L  D  V  E  H  R  T  V  A  -

   TGGAGTCCTGAGCAGCACCTTCTGGACAGGGGGCGTGATGCTGCTGGCACTGGTTGGGTA
721 ---------+---------+---------+---------+---------+---------+ 780
   ACCTCAGGACTCGTCGTGGAAGACCTGTCCCCCGCACTACGACGACCGTGACCAACCCAT

    G  V  L  S  S  T  F  W  T  G  G  V  M  L  L  A  L  V  G  Y  -

   CCTGATACGGGACTGGCGATGGCTTCTGCTAGCTGTCACCCTGCCTTGTGCCCCAAGCAT
781 ---------+---------+---------+---------+---------+---------+ 840
   GGACTATGCCCTGACCGCTACCGAAGACGATCGACAGTGGGACGGAACACGGGGTTCGTA

    L  I  R  D  W  R  W  L  L  L  A  V  T  L  P  C  A  P  S  I  -

   CCTCAGCCTCTGGTGGGTGCCTGAGTCTGCACGCTGGCTTCTGACCCAAGGCCATGTGAA
841 ---------+---------+---------+---------+---------+---------+ 900
   GGAGTCGGAGACCACCCACGGACTCAGACGTGCGACCGAAGACTGGGTTCCGGTACACTT

    L  S  L  W  W  V  P  E  S  A  R  W  L  L  T  Q  G  H  V  K  -

   AGAGGCCCACAGGTACTTGCTCCACTGTGCCAGGCTCAATGGGCGGCCAGTGTGTGAGGA
901 ---------+---------+---------+---------+---------+---------+ 960
   TCTCCGGGTGTCCATGAACGAGGTGACACGGTCCGAGTTACCCGCCGGTCACACACTCCT

    E  A  H  R  Y  L  L  H  C  A  R  L  N  G  R  P  V  C  E  D  -

   CAGCTTCAGCCAGGAGGCTGTGAGCAAAGTGGCCGCCGGGGAACGGGTGGTCCGAAGACC
961 ---------+---------+---------+---------+---------+---------+ 1020
   GTCGAAGTCGGTCCTCCGACACTCGTTTCACCGGCGGCCCCTTGCCCACCAGGCTTCTGG

    S  F  S  Q  E  A  V  S  K  V  A  A  G  E  R  V  V  R  R  P  -

   TTCATACCTAGACCTGTTCCGCACACCACGGCTCCGACACATCTCACTGTGCTGCGTGGT
1021 ---------+---------+---------+---------+---------+---------+ 1080
   AAGTATGGATCTGGACAAGGCGTGTGGTGCCGAGGCTGTGTAGAGTGACACGACGCACCA

    S  Y  L  D  L  F  R  T  P  R  L  R  H  I  S  L  C  C  V  V  -
```

FIGURE 2

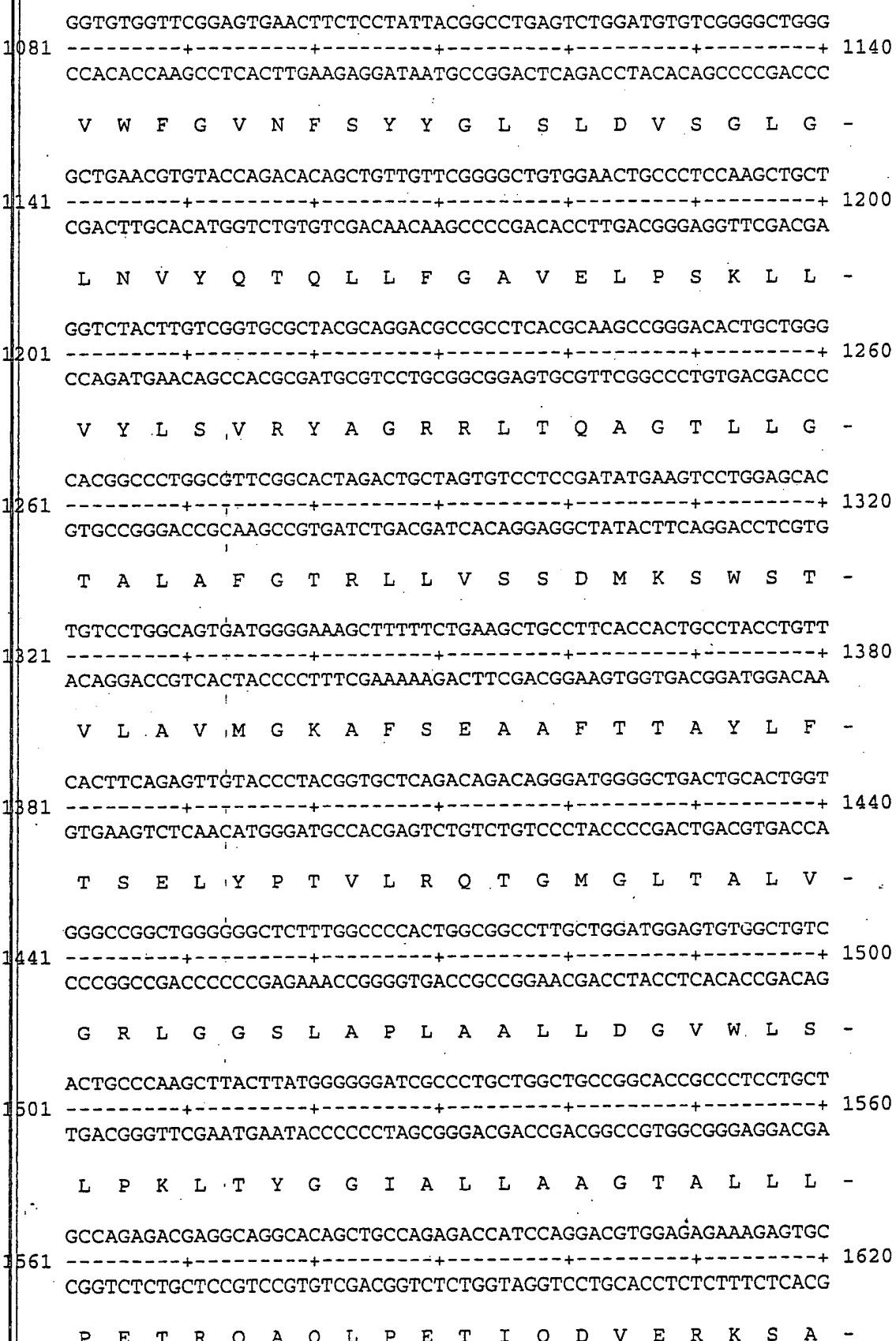

GGTGTGGTTCGGAGTGAACTTCTCCTATTACGGCCTGAGTCTGGATGTGTCGGGGCTGGG
1081 + 1140
CCACACCAAGCCTCACTTGAAGAGGATAATGCCGGACTCAGACCTACACAGCCCCGACCC
V W F G V N F S Y Y G L S L D V S G L G -
GCTGAACGTGTACCAGACACAGCTGTTGTTCGGGGCTGTGGAACTGCCCTCCAAGCTGCT
1141 + 1200
CGACTTGCACATGGTCTGTGTCGACAACAAGCCCCGACACCTTGACGGGAGGTTCGACGA
L N V Y Q T Q L L F G A V E L P S K L L -
GGTCTACTTGTCGGTGCGCTACGCAGGACGCCGCCTCACGCAAGCCGGGACACTGCTGGG
1201 + 1260
CCAGATGAACAGCCACGCGATGCGTCCTGCGGCGGAGTGCGTTCGGCCCTGTGACGACCC
V Y L S V R Y A G R R L T Q A G T L L G -
CACGGCCCTGGCGTTCGGCACTAGACTGCTAGTGTCCTCCGATATGAAGTCCTGGAGCAC
1261 + 1320
GTGCCGGGACCGCAAGCCGTGATCTGACGATCACAGGAGGCTATACTTCAGGACCTCGTG
T A L A F G T R L L V S S D M K S W S T -
TGTCCTGGCAGTGATGGGGAAAGCTTTTTCTGAAGCTGCCTTCACCACTGCCTACCTGTT
1321 + 1380
ACAGGACCGTCACTACCCCTTTCGAAAAAGACTTCGACGGAAGTGGTGACGGATGGACAA
V L A V M G K A F S E A A F T T A Y L F -
CACTTCAGAGTTGTACCCTACGGTGCTCAGACAGACAGGGATGGGGCTGACTGCACTGGT
1381 + 1440
GTGAAGTCTCAACATGGGATGCCACGAGTCTGTCTGTCCCTACCCCGACTGACGTGACCA
T S E L Y P T V L R Q T G M G L T A L V -
GGGCCGGCTGGGGGGCTCTTTGGCCCCACTGGCGGCCTTGCTGGATGGAGTGTGGCTGTC
1441 + 1500
CCCGGCCGACCCCCCGAGAAACCGGGGTGACCGCCGGAACGACCTACCTCACACCGACAG
G R L G G S L A P L A A L L D G V W L S -
ACTGCCCAAGCTTACTTATGGGGGGATCGCCCTGCTGGCTGCCGGCACCGCCCTCCTGCT
1501 + 1560
TGACGGGTTCGAATGAATACCCCCCTAGCGGGACGACCGACGGCCGTGGCGGGAGGACGA
L P K L T Y G G I A L L A A G T A L L L -
GCCAGAGACGAGGCAGGCACAGCTGCCAGAGACCATCCAGGACGTGGAGAGAAAGAGTGC
1561 + 1620
CGGTCTCTGCTCCGTCCGTGTCGACGGTCTCTGGTAGGTCCTGCACCTCTCTTTCTCACG
P E T R Q A Q L P E T I Q D V E R K S A -

FIGURE 2

```
    CCCAACCAGTCTTCAGGAGGAAGAGATGCCCATGAAGCAGGTCCAGAACTAAGTGGGAGT
1621 ---------+---------+---------+---------+---------+---------+ 1680
    GGGTTGGTCAGAAGTCCTCCTTCTCTACGGGTACTTCGTCCAGGTCTTGATTCACCCTCA

     P   T   S   L   Q   E   E   E   M   P   M   K   Q   V   Q   N   *

    GGAGGCAGGCCCTCCACAGAAGCTCTGCAGCAGGGGCTGGGAGAGCAGAAGGGCAGGCCC
1681 ---------+---------+---------+---------+---------+---------+ 1740
    CCTCCGTCCGGGAGGTGTCTTCGAGACGTCGTCCCCGACCCTCTCGTCTTCCCGTCCGGG

    TGCAACTCAGGCTGGGAGTATCGAACCCTCTGCCTAGGGCCGGAGTTGCTGCCAGTACCC
1741 ---------+---------+---------+---------+---------+---------+ 1800
    ACGTTGAGTCCGACCCTCATAGCTTGGGAGACGGATCCCGGCCTCAACGACGGTCATGGG

    GCTCCCTCTGCTCATCCATCCTTGATTATTTGGCTTCTAGGAACAGTTGACTTCCCAGAA
1801 ---------+---------+---------+---------+---------+---------+ 1860
    CGAGGGAGACGAGTAGGTAGGAACTAATAAACCGAAGATCCTTGTCAACTGAAGGGTCTT

    TGCAGTGGGCTGCTGGGCACCCCTCTCACGGTTGGGGAGGATTCTGTAAATAAAGGTGCC
1861 ---------+---------+---------+---------+---------+---------+ 1920
    ACGTCACCCGACGACCCGTGGGGAGAGTGCCAACCCCTCCTAAGACATTTATTTCCACGG

    CCTTGGGTTGGGGCAATGGTGACGAGCTGTGGGAAGAGCCCTGGATAGGAAGCCACTGAG
1921 ---------+---------+---------+---------+---------+---------+ 1980
    GGAACCCAACCCCGTTACCACTGCTCGACACCCTTCTCGGGACCTATCCTTCGGTGACTC

    TCTGCCCTGGGCTCTGATAAAACCTTCACCATTAACTTGCTGTGTGACCTTGGGCATGTG
1981 ---------+---------+---------+---------+---------+---------+ 2040
    AGACGGGACCCGAGACTATTTTGGAAGTGGTAATTGAACGACACACTGGAACCCGTACAC

    GCTTTCCCTCTCTGGCCTCAGTCTGTTCATCTCCCAAATGGATAATGAAGCCTCTTGGGA
2041 ---------+---------+---------+---------+---------+---------+ 2100
    CGAAAGGGAGAGACCGGAGTCAGACAAGTAGAGGGTTTACCTATTACTTCGGAGAACCCT

    GGCCCTACCATAGGATCTGTTGCCATGCTCAAATGAGTTACTGAATAAGGTGCTTCTGCT
2101 ---------+---------+---------+---------+---------+---------+ 2160
    CCGGGATGGTATCCTAGACAACGGTACGAGTTTACTCAATGACTTATTCCACGAAGACGA

    TCTTCTAGAGATGGTGCTAAAGAAAGGACTAGCATATGAGACTTCTGGTACCAATGGGGC
2161 ---------+---------+---------+---------+---------+---------+ 2220
    AGAAGATCTCTACCACGATTTCTTTCCTGATCGTATACTCTGAAGACCATGGTTACCCCG

    TGGTGGGCATGCTGTCCACTGTGTGGTGCTAGGACTGCCAATGCCAGGCCCAAGGGACAA
2221 ---------+---------+---------+---------+---------+---------+ 2280
    ACCACCCGTACGACAGGTGACACACCACGATCCTGACGGTTACGGTCCGGGTTCCCTGTT

    AAAGAACAGAGCTTTTTGTTCTCATGGCTGGCCCTGCTACCTCCGAGGCACCCTGCAGGG
2281 ---------+---------+---------+---------+---------+---------+ 2340
    TTTCTTGTCTCGAAAAACAAGAGTACCGACCGGGACGATGGAGGCTCCGTGGGACGTCCC

    CAATGCATGTCATCCCAACCCCCACACTCCCCATCCTCCAACCCACTGGTCTCATGCCCA
2341 ---------+---------+---------+---------+---------+---------+ 2400
    GTTACGTACAGTAGGGTTGGGGGTGTGAGGGGTAGGAGGTTGGGTGACCAGAGTACGGGT
```

FIGURE 2

```
    AAGAAGAGTTGAAGGCATGGGAGCCAACATTTTATTGAAGAAGCCACAGAGGCTGAAATT
2401 ---------+---------+---------+---------+---------+---------+ 2460
    TTCTTCTCAACTTCCGTACCCTCGGTTGTAAAATAACTTCTTCGGTGTCTCCGACTTTAA

    CAATAAACACAAGTTTTATGAGTAAAAAAAAAAAAAAAAAA
2461 ---------+---------+---------+---------+- 2501
    GTTATTTGTGTTCAAAATACTCATTTTTTTTTTTTTTTTT
```

FIGURE 2

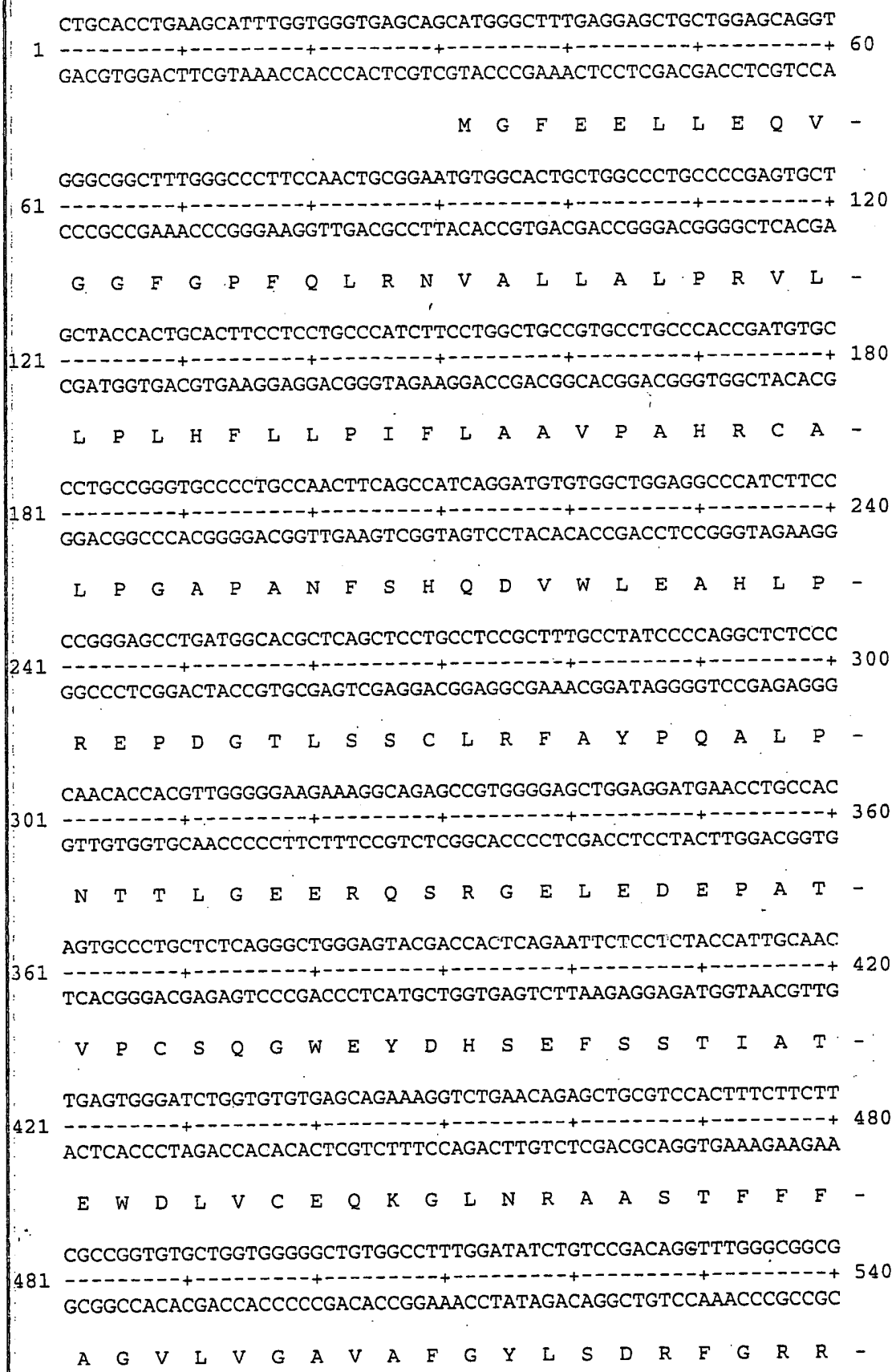


FIGURE 3
Sheet 1 of 4

```
    GCGTCTGCTGCTGGTAGCCTACGTGAGTACCCTGGTGCTGGGCCTGGCATCTGCAGCCTC
541 ---------+---------+---------+---------+---------+---------+ 600
    CGCAGACGACGACCATCGGATGCACTCATGGGACCACGACCCGGACCGTAGACGTCGGAG

     R  L  L  L  V  A  Y  V  S  T  L  V  L  G  L  A  S  A  A  S  -

    CGTCAGCTATGTAATGTTTGCCATCACCCGCACCCTTACTGGCTCAGCCCTGGCTGGTTT
601 ---------+---------+---------+---------+---------+---------+ 660
    GCAGTCGATACATTACAAACGGTAGTGGGCGTGGGAATGACCGAGTCGGGACCGACCAAA

     V  S  Y  V  M  F  A  I  T  R  T  L  T  G  S  A  L  A  G  F  -

    TACCATCATCGTGATGCCACTGGAGCTGGAGTGGCTGGATGTGGAGCACCGCACCGTGGC
661 ---------+---------+---------+---------+---------+---------+ 720
    ATGGTAGTAGCACTACGGTGACCTCGACCTCACCGACCTACACCTCGTGGCGTGGCACCG

     T  I  I  V  M  P  L  E  L  E  W  L  D  V  E  H  R  T  V  A  -

    TGGAGTCCTGAGCAGCACCTTCTGGACAGGGGGCGTGATGCTGCTGGCACTGGTTGGGTA
721 ---------+---------+---------+---------+---------+---------+ 780
    ACCTCAGGACTCGTCGTGGAAGACCTGTCCCCCGCACTACGACGACCGTGACCAACCCAT

     G  V  L  S  S  T  F  W  T  G  G  V  M  L  L  A  L  V  G  Y  -

    CCTGATACGGGACTGGCGATGGCTTCTGCTAGCTGTCACCCTGCCTTGTGCCCCAAGCAT
781 ---------+---------+---------+---------+---------+---------+ 840
    GGACTATGCCCTGACCGCTACCGAAGACGATCGACAGTGGGACGGAACACGGGGTTCGTA

     L  I  R  D  W  R  W  L  L  L  A  V  T  L  P  C  A  P  S  I  -

    CCTCAGCCTCTGGTGGGTGCCTGAGTCTGCACGCTGGCTTCTGACCCAAGGCCATGTGAA
841 ---------+---------+---------+---------+---------+---------+ 900
    GGAGTCGGAGACCACCCACGGACTCAGACGTGCGACCGAAGACTGGGTTCCGGTACACTT

     L  S  L  W  W  V  P  E  S  A  R  W  L  L  T  Q  G  H  V  K  -

    AGAGGCCCACAGGTACTTGCTCCACTGTGCCAGGCTCAATGGGCGGCCAGTGTGTGAGGA
901 ---------+---------+---------+---------+---------+---------+ 960
    TCTCCGGGTGTCCATGAACGAGGTGACACGGTCCGAGTTACCCGCCGGTCACACACTCCT

     E  A  H  R  Y  L  L  H  C  A  R  L  N  G  R  P  V  C  E  D  -

    CAGCTTCAGCCAGGAGGCTGTGAGCAAAGTGGCCGCCGGGGAACGGGTGGTCCGAAGACC
961 ---------+---------+---------+---------+---------+---------+ 1020
    GTCGAAGTCGGTCCTCCGACACTCGTTTCACCGGCGGCCCCTTGCCCACCAGGCTTCTGG

     S  F  S  Q  E  A  V  S  K  V  A  A  G  E  R  V  V  R  R  P  -

    TTCATACCTAGACCTGTTCCGCACACCACGGCTCCGACACATCTCACTGTGCTGCGTGGT
1021 ---------+---------+---------+---------+---------+---------+ 1080
    AAGTATGGATCTGGACAAGGCGTGTGGTGCCGAGGCTGTGTAGAGTGACACGACGCACCA

     S  Y  L  D  L  F  R  T  P  R  L  R  H  I  S  L  C  C  V  V  -
```

FIGURE 3
Sheet 2 of 4

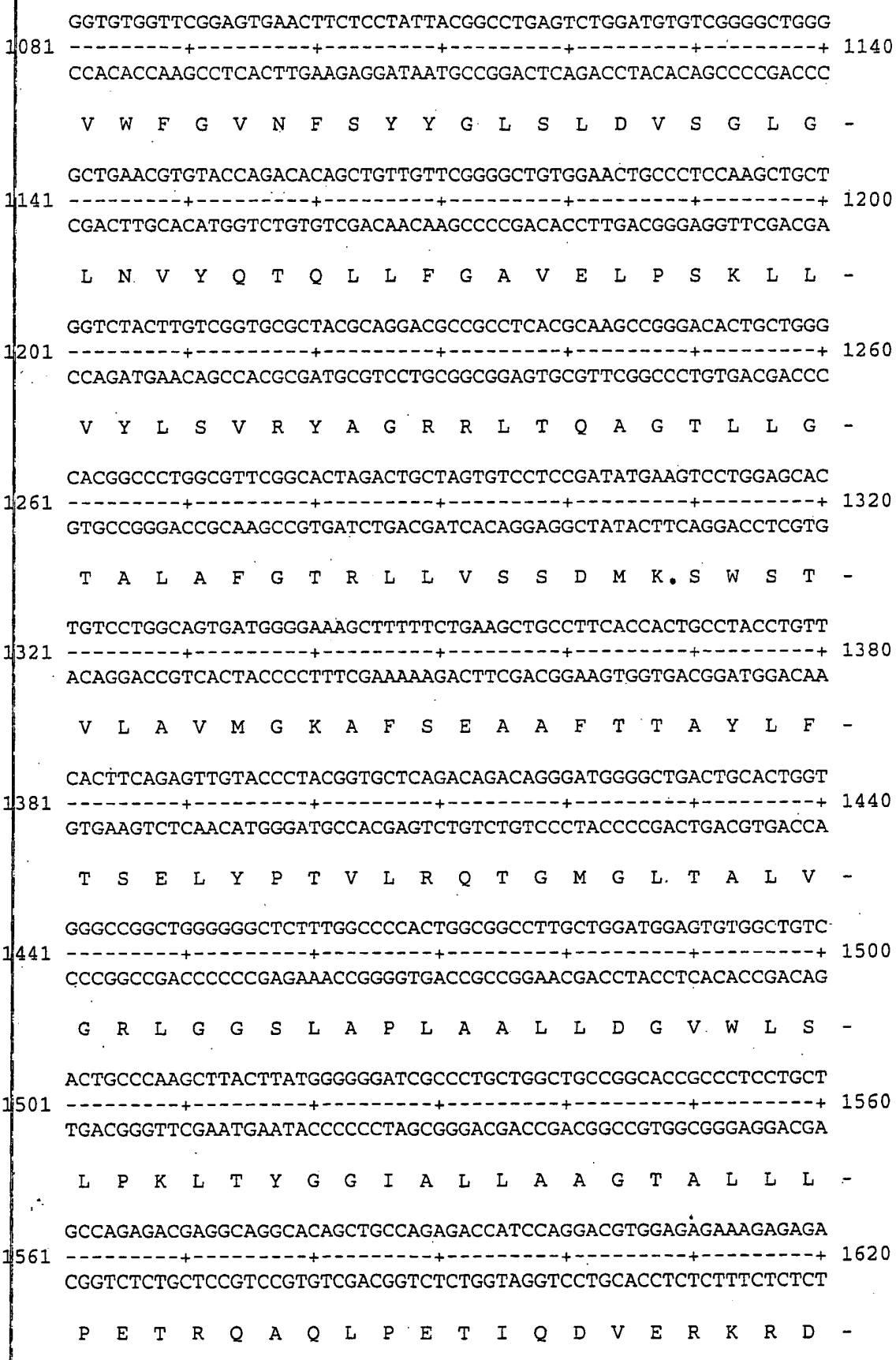


FIGURE 3
Sheet 3 of 4

```
    TGGTGCTAAAGAAAGGACTAGCATATGAGACTTCTGGTACCAATGGGGCTGGTGGGCATG
1621 ---------+---------+---------+---------+---------+---------+ 1680
    ACCACGATTTCTTTCCTGATCGTATACTCTGAAGACCATGGTTACCCCGACCACCCGTAC

     G  A  K  E  R  T  S  I  *

    CTGTCCACTGTGTGGTGCTAGGACTGCCAATGCCAGGCCCAAGGGACAAAAAGAACAGAG
1681 ---------+---------+---------+---------+---------+---------+ 1740
    GACAGGTGACACACCACGATCCTGACGGTTACGGTCCGGGTTCCCTGTTTTTCTTGTCTC

    CTTTTTGTTCTCATGGCTGGCCCTGCTACCTCCGAGGCACCCTGCAGGGCAATGCATGTC
1741 ---------+---------+---------+---------+---------+---------+ 1800
    GAAAAACAAGAGTACCGACCGGGACGATGGAGGCTCCGTGGGACGTCCCGTTACGTACAG

    ATCCCAACCCCCACACTCCCCATCCTCCAACCCACTGGTCTCATGCCCAAAGAAGAGTTG
1801 ---------+---------+---------+---------+---------+---------+ 1860
    TAGGGTTGGGGGTGTGAGGGGTAGGAGGTTGGGTGACCAGAGTACGGGTTTCTTCTCAAC

    AAGGCATGGGAGCCAACATTTTATTGAAGAAGCCACAGAGGCTGAAATTCAATAAACACA
1861 ---------+---------+---------+---------+---------+---------+ 1920
    TTCCGTACCCTCGGTTGTAAAATAACTTCTTCGGTGTCTCCGACTTTAAGTTATTTGTGT

    AGTTTTATGAGTAAAAAAAAAAAAAAAAA
1921 ---------+---------+---------+ 1950
    TCAAAATACTCATTTTTTTTTTTTTTTTT
```

FIGURE 3
Sheet 4 of 4

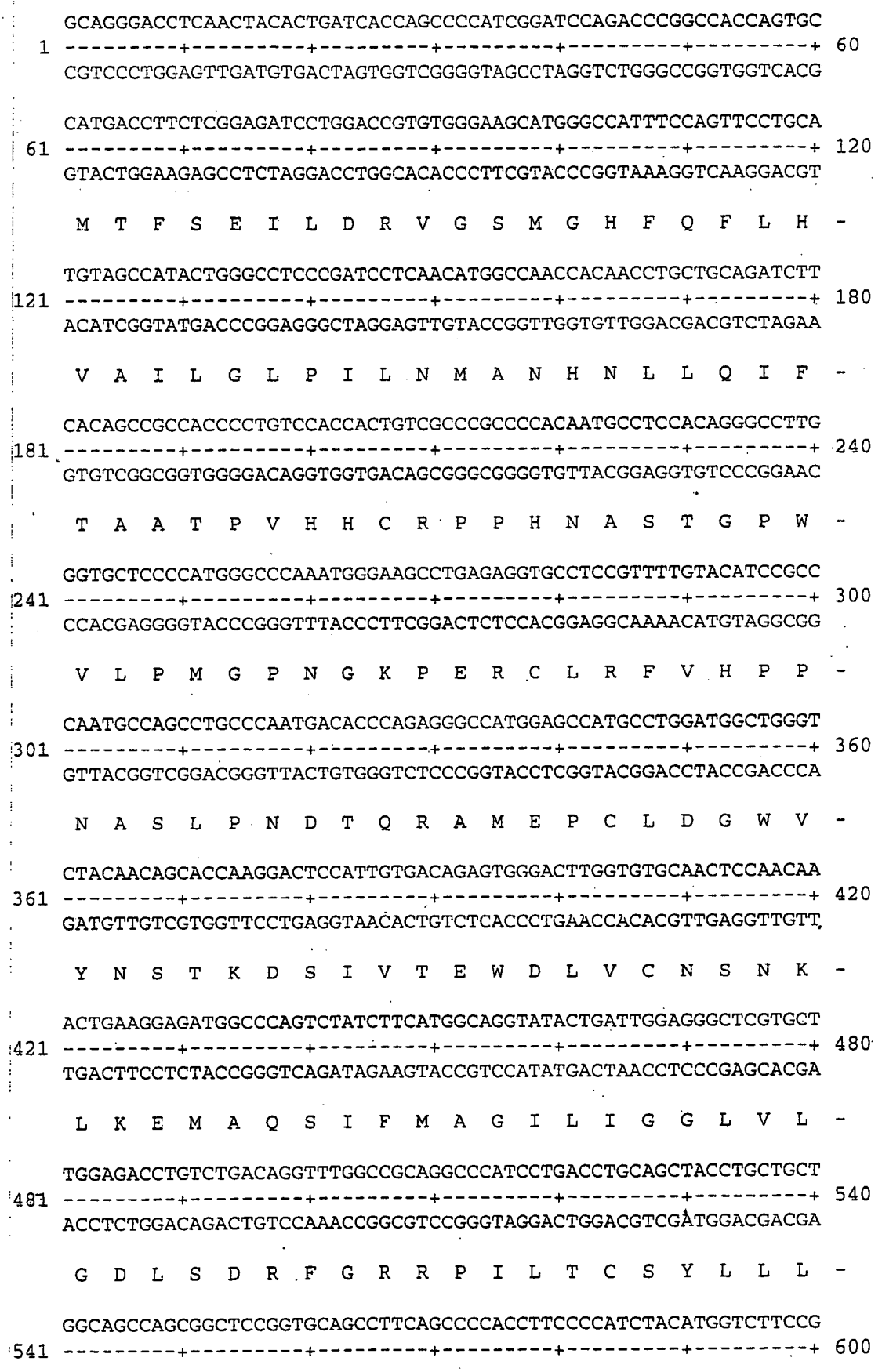


FIGURE 4
Sheet 1 of 4

```
    CCGTCGGTCGCCGAGGCCACGTCGGAAGTCGGGGTGGAAGGGGTAGATGTACCAGAAGGC

     A  A  S  G  S  G  A  A  F  S  P  T  F  P  I  Y  M  V  F  R  -

    CTTCCTGTGTGGCTTTGGCATCTCAGGCATTACCCTGAGCACCGTCATCTTGAATGTGGA
601 ---------+---------+---------+---------+---------+---------+ 660
    GAAGGACACACCGAAACCGTAGAGTCCGTAATGGGACTCGTGGCAGTAGAACTTACACCT

     F  L  C  G  F  G  I  S  G  I  T  L  S  T  V  I  L  N  V  E  -

    ATGGGTGCCTACCCGGATGCGGGCCATCATGTCGACAGCACTCGGGTACTGCTACACCTT
661 ---------+---------+---------+---------+---------+---------+ 720
    TACCCACGGATGGGCCTACGCCCGGTAGTACAGCTGTCGTGAGCCCATGACGATGTGGAA

     W  V  P  T  R  M  R  A  I  M  S  T  A  L  G  Y  C  Y  T  F  -

    TGGCCAGTTCATTCTGCCCGGCCTGGCCTACGCCATCCCCCAGTGGCGTTGGCTGCAGTT
721 ---------+---------+---------+---------+---------+---------+ 780
    ACCGGTCAAGTAAGACGGGCCGGACCGGATGCGGTAGGGGGTCACCGCAACCGACGTCAA

     G  Q  F  I  L  P  G  L  A  Y  A  I  P  Q  W  R  W  L  Q  L  -

    AACTGTGTCCATTCCCTTCTTCGTCTTCTTCCTATCATCCTGGTGGACACCAGAGTCCAT
781 ---------+---------+---------+---------+---------+---------+ 840
    TTGACACAGGTAAGGGAAGAAGCAGAAGAAGGATAGTAGGACCACCTGTGGTCTCAGGTA

     T  V  S  I  P  F  F  V  F  F  L  S  S  W  W  T  P  E  S  I  -

    ACGCTGGTTGGTCTTGTCTGGAAAGTCCTCGAAGGCCCTGAAGATACTCCGGCGGGTGGC
841 ---------+---------+---------+---------+---------+---------+ 900
    TGCGACCAACCAGAACAGACCTTTCAGGAGCTTCCGGGACTTCTATGAGGCCGCCCACCG

     R  W  L  V  L  S  G  K  S  S  K  A  L  K  I  L  R  R  V  A  -

    TGTCTTCAATGGCAAGAAGGAAGAGGGAGAAAGGCTCAGCTTGGAGGAGCTCAAACTCAA
901 ---------+---------+---------+---------+---------+---------+ 960
    ACAGAAGTTACCGTTCTTCCTTCTCCCTCTTTCCGAGTCGAACCTCCTCGAGTTTGAGTT

     V  F  N  G  K  K  E  E  G  E  R  L  S  L  E  E  L  K  L  N  -

    CCTGCAGAAGGAGATCTCCTTGGCCAAGGCCAAGTACACCGCAAGTGACCTGTTCCGGAT
961 ---------+---------+---------+---------+---------+---------+ 1020
    GGACGTCTTCCTCTAGAGGAACCGGTTCCGGTTCATGTGGCGTTCACTGGACAAGGCCTA

     L  Q  K  E  I  S  L  A  K  A  K  Y  T  A  S  D  L  F  R  I  -

    ACCCATGCTGCGCCGCATGACCTTCTGTCTTTCCCTGGCCTGGTTTGCTACCGGTTTTGC
1021 ---------+---------+---------+---------+---------+---------+ 1080
    TGGGTACGACGCGGCGTACTGGAAGACAGAAAGGGACCGGACCAAACGATGGCCAAAACG

     P  M  L  R  R  M  T  F  C  L  S  L  A  W  F  A  T  G  F  A  -

    CTACTATAGTTTGGCTATGGGTGTGGAAGAATTTGGAGTCAACCTCTACATCCTCCAGAT
1081 ---------+---------+---------+---------+---------+---------+ 1140
```

FIGURE 4
Sheet 2 of 4

```
      GATGATATCAAACCGATACCCACACCTTCTTAAACCTCAGTTGGAGATGTAGGAGGTCTA

       Y  Y  S  L  A  M  G  V  E  E  F  G  V  N  L  Y  I  L  Q  I  -

      CATCTTTGGTGGGGTCGATGTCCCAGCCAAGTTCATCACCATCCTCTCCTTAAGCTACCT
1141  ---------+---------+---------+---------+---------+---------+ 1200
      GTAGAAACCACCCCAGCTACAGGGTCGGTTCAAGTAGTGGTAGGAGAGGAATTCGATGGA

       I  F  G  G  V  D  V  P  A  K  F  I  T  I  L  S  L  S  Y  L  -

      GGGCCGGCATACCACTCAGGCCGCTGCCCTGCTCCTGGCAGGAGGGGCCATCTTGGCTCT
1201  ---------+---------+---------+---------+---------+---------+ 1260
      CCCGGCCGTATGGTGAGTCCGGCGACGGGACGAGGACCGTCCTCCCCGGTAGAACCGAGA

       G  R  H  T  T  Q  A  A  A  L  L  L  A  G  G  A  I  L  A  L  -

      CACCTTTGTGCCCTTGGACTTGCAGACCGTGAGGACAGTATTGGCTGTGTTTGGGAAGGG
1261  ---------+---------+---------+---------+---------+---------+ 1320
      GTGGAAACACGGGAACCTGAACGTCTGGCACTCCTGTCATAACCGACACAAACCCTTCCC

       T  F  V  P  L  D  L  Q  T  V  R  T  V  L  A  V  F  G  K  G  -

      ATGCCTATCCAGCTCCTTCAGCTGCCTCTTCCTCTACACAAGTGAATTATACCCCACAGT
1321  ---------+---------+---------+---------+---------+---------+ 1380
      TACGGATAGGTCGAGGAAGTCGACGGAGAAGGAGATGTGTTCACTTAATATGGGGTGTCA

       C  L  S  S  S  F  S  C  L  F  L  Y  T  S  E  L  Y  P  T  V  -

      CATCAGGCAAACAGGTATGGGCGTAAGTAACCTGTGGACCCGCGTGGGAAGCATGGTGTC
1381  ---------+---------+---------+---------+---------+---------+ 1440
      GTAGTCCGTTTGTCCATACCCGCATTCATTGGACACCTGGGCGCACCCTTCGTACCACAG

       I  R  Q  T  G  M  G  V  S  N  L  W  T  R  V  G  S  M  V  S  -

      CCCGCTGGTGAAAATCACGGGTGAGGTACAGCCCTTCATCCCCAATATCATCTACGGGAT
1441  ---------+---------+---------+---------+---------+---------+ 1500
      GGGCGACCACTTTTAGTGCCCACTCCATGTCCGGAAGTAGGGGTTATAGTAGATGCCCTA

       P  L  V  K  I  T  G  E  V  Q  P  F  I  P  N  I  I  Y  G  I  -

      CACCGCCCTCCTCGGGGGCAGTGCTGCCCTCTTCCTGCCTGAGACCCTGAATCAGCCCTT
1501  ---------+---------+---------+---------+---------+---------+ 1560
      GTGGCGGGAGGAGCCCCCGTCACGACGGGAGAAGGACGGACTCTGGGACTTAGTCGGGAA

       T  A  L  L  G  G  S  A  A  L  F  L  P  E  T  L  N  Q  P  L  -

      GCCAGAGACTATCGAAGACCTGGAAAACTGGTCCCTGCGGGCAAAGAAGCCAAAGCAGGA
1561  ---------+---------+---------+---------+---------+---------+ 1620
      CGGTCTCTGATAGCTTCTGGACCTTTTGACCAGGGACGCCCGTTTCTTCGGTTTCGTCCT

       P  E  T  I  E  D  L  E  N  W  S  L  R  A  K  K  P  K  Q  E  -

      GCCAGAGGTGGAAAAGGCCTCCCAGAGGATCCCTCTACAGCCTCACGGACCAGGCCTGGG
1621  ---------+---------+---------+---------+---------+---------+ 1680
```

FIGURE 4
Sheet 3 of 4

```
     CGGTCTCCACCTTTTCCGGAGGGTCTCCTAGGGAGATGTCGGAGTGCCTGGTCCGGACCC

      P  E  V  E  K  A  S  Q  R  I  P  L  Q  P  H  G  P  G  L  G  -

     CTCCAGCTGAGGACAACGGAACCCCCTTTCCCTGCCCTCCAGAGACTGATCCTAGCCAGG
1681 ---------+---------+---------+---------+---------+---------+ 1740
     GAGGTCGACTCCTGTTGCCTTGGGGGAAAGGGACGGGAGGTCTCTGACTAGGATCGGTCC

      S  S  *

     CACCTTAGGAGTATAGGGAGGCCCCATATAGGTCCATCCTCCTAGGATGAAGCCTTCTGA
1741 ---------+---------+---------+---------+---------+---------+ 1800
     GTGGAATCCTCATATCCCTCCGGGGTATATCCAGGTAGGAGGATCCTACTTCGGAAGACT

     GAGCTTGGTGAAGGTGTCTCCATCACCACCACCAGAGCCTCCTGCCCAGCCCTGGCCAGT
1801 ---------+---------+---------+---------+---------+---------+ 1860
     CTCGAACCACTTCCACAGAGGTAGTGGTGGTGGTCTCGGAGGACGGGTCGGGACCGGTCA

     TCAAAGGTTCAAGCCATCCCTGCCCTTGTTCTCCCTGCAACCCAAGCCCTGCCATTCTTC
1861 ---------+---------+---------+---------+---------+---------+ 1920
     AGTTTCCAAGTTCGGTAGGGACGGGAACAAGAGGGACGTTGGGTTCGGGACGGTAAGAAG

     TGTCTAGCCCTTCCCCACTGGCCAACTTCCCCCACTGTCCCGGTCCTCTTCCCCTGAGGT
1921 ---------+---------+---------+---------+---------+---------+ 1980
     ACAGATCGGGAAGGGGTGACCGGTTGAAGGGGGTGACAGGGCCAGGAGAAGGGGACTCCA

     CCCCTGATATCCCCTGGCTCAGTCCTAACAAGACTGAGTCTTAACAAGATGAGAAGTCCT
1981 ---------+---------+---------+---------+---------+---------+ 2040
     GGGGACTATAGGGGACCGAGTCAGGATTGTTCTGACTCAGAATTGTTCTACTCTTCAGGA

     CCCCTTCTTGCCTCCCACACTTTTCTTTGATGGGAGGTTTCAATAAACAGCGATAAGAAC
2041 ---------+---------+---------+---------+---------+---------+ 2100
     GGGGAAGAACGGAGGGTGTGAAAAGAAACTACCCTCCAAAGTTATTTGTCGCTATTCTTG

     TCTAAAAAAAAAAAAAAAAA
2101 ---------+---------+- 2121
     AGATTTTTTTTTTTTTTTTT
```

FIGURE 4
Sheet 4 of 4

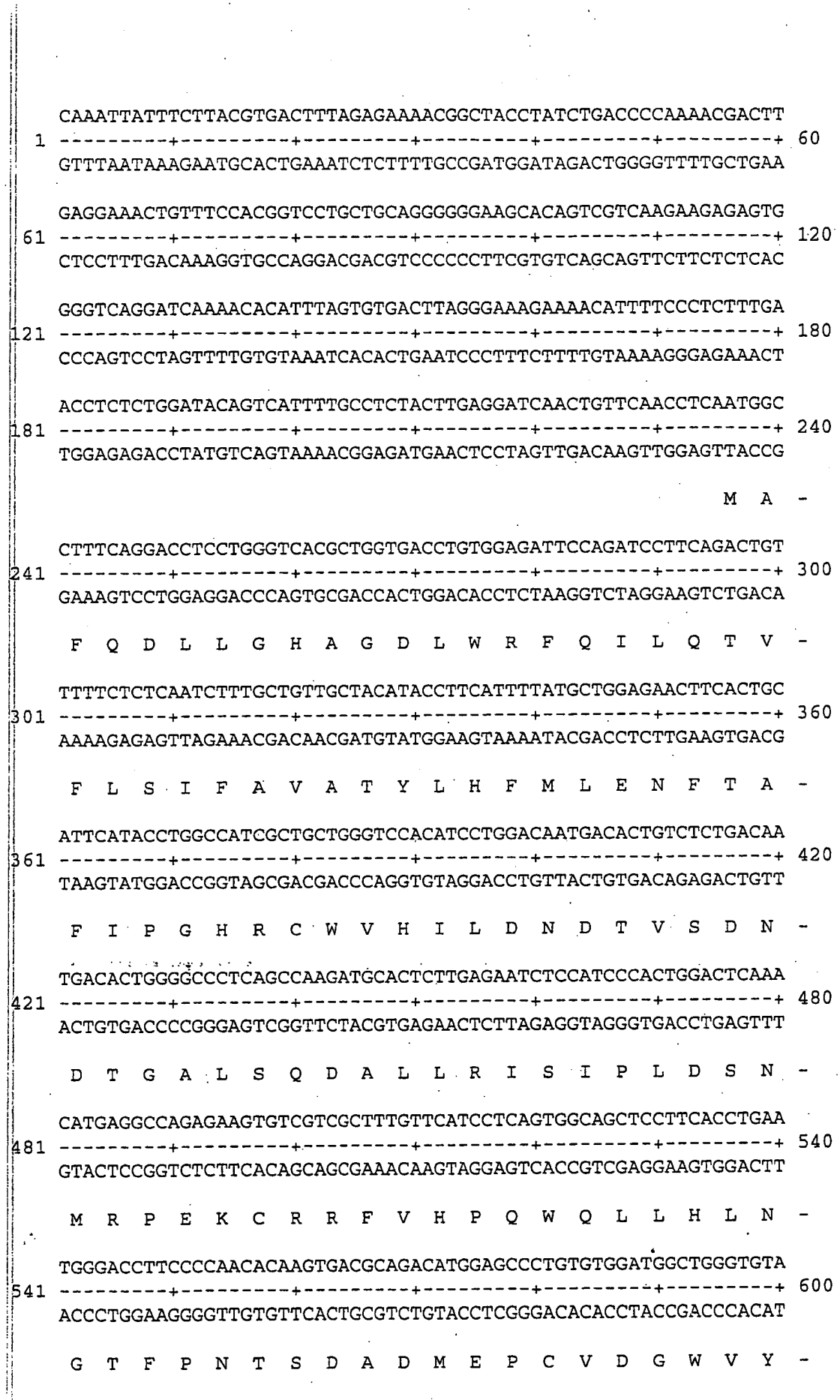


FIGURE 5
Sheet 1 of 4

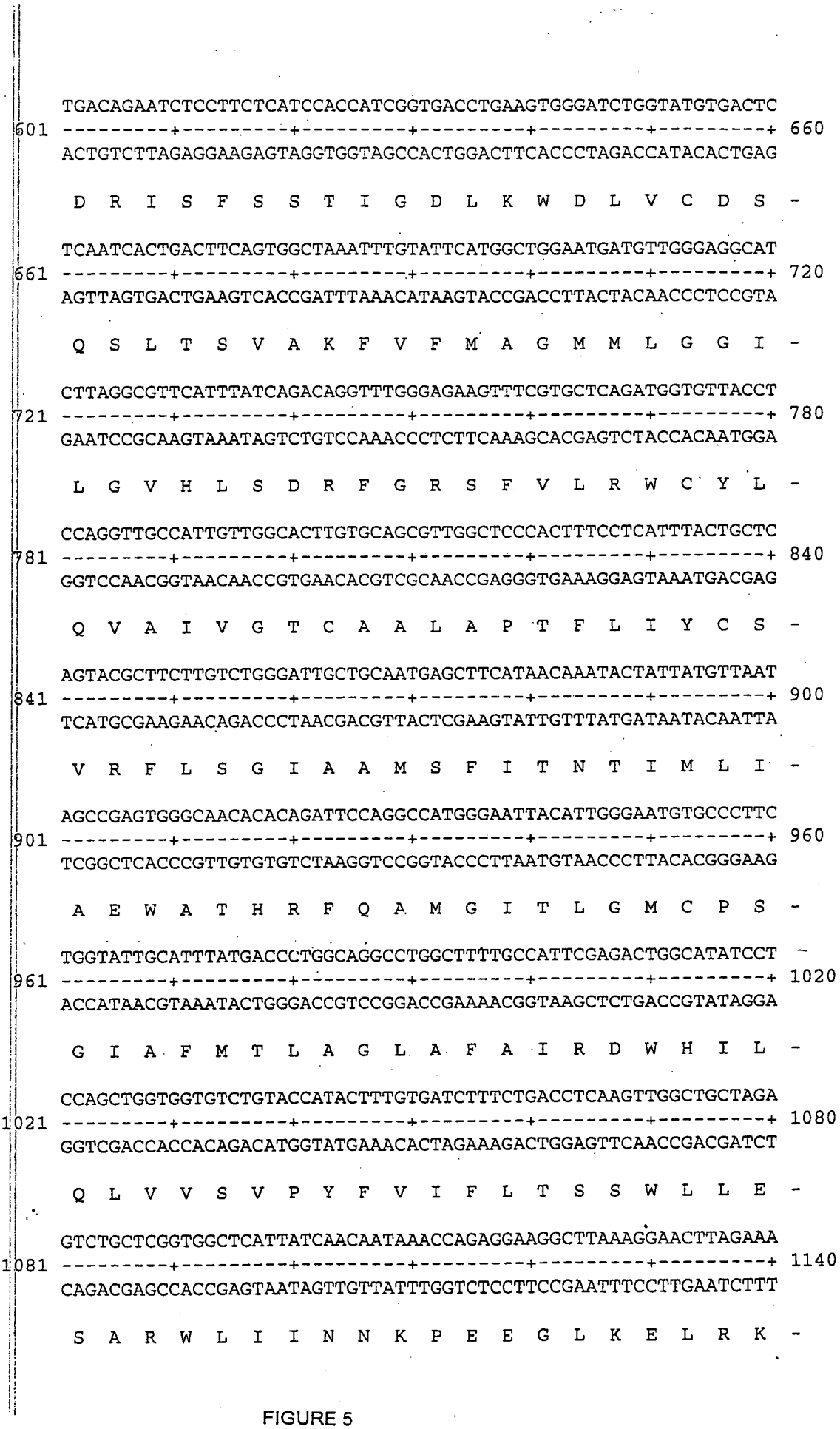


FIGURE 5
Sheet 2 of 4

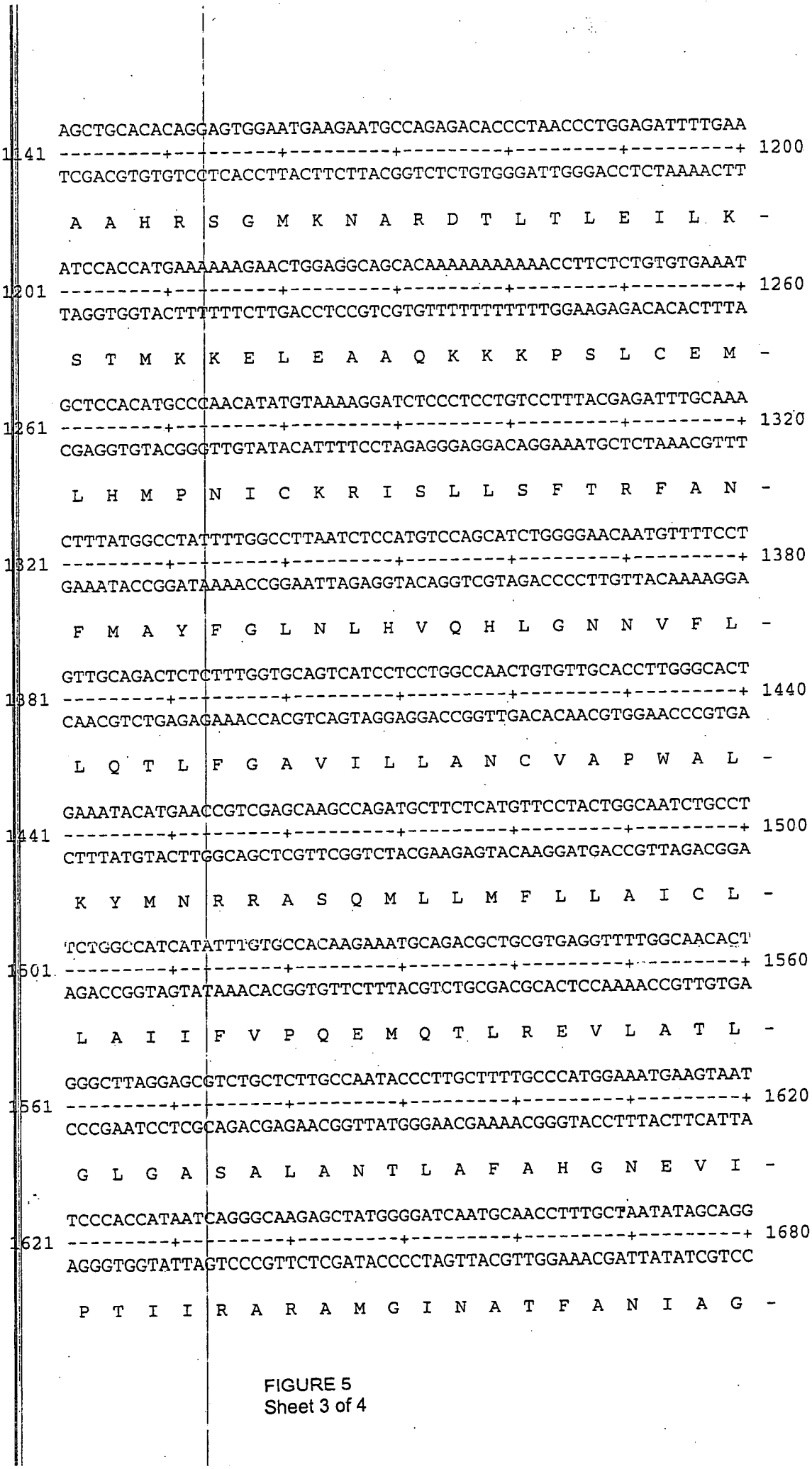


FIGURE 5
Sheet 3 of 4

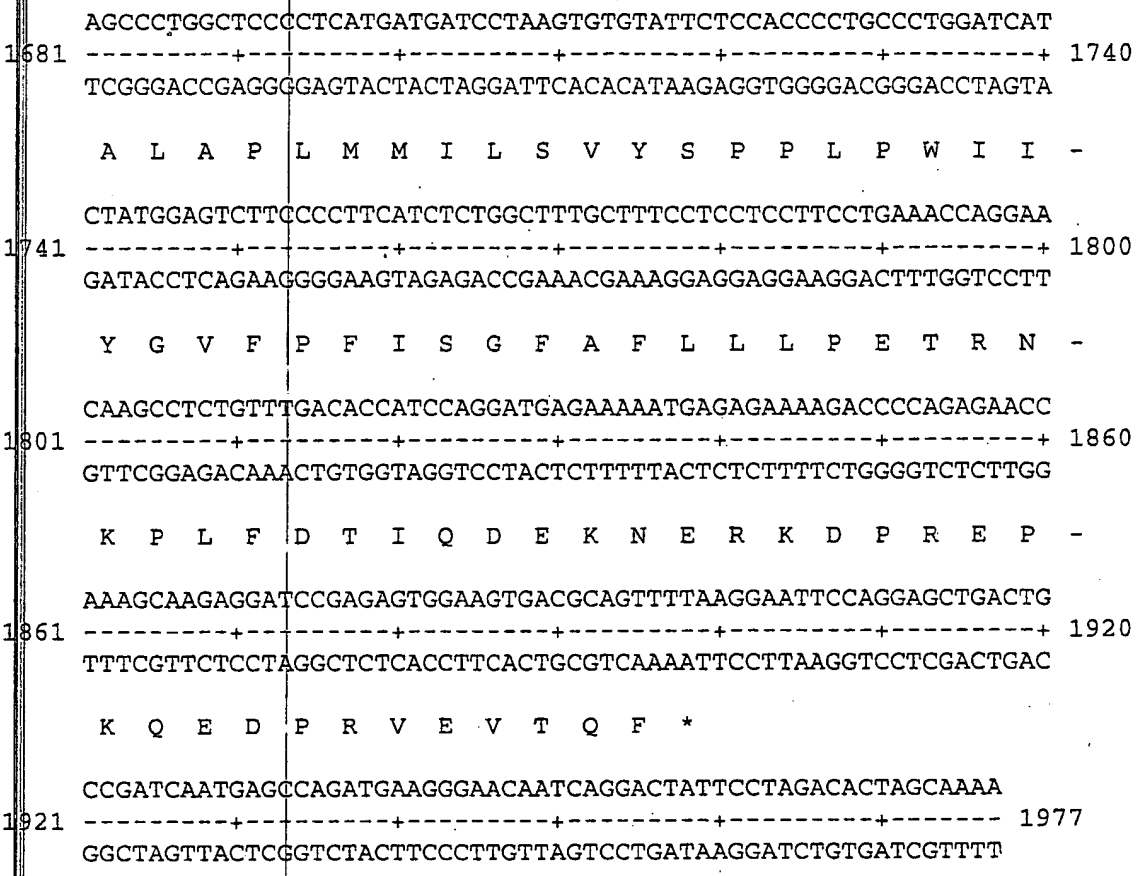


FIGURE 5
Sheet 4 of 4

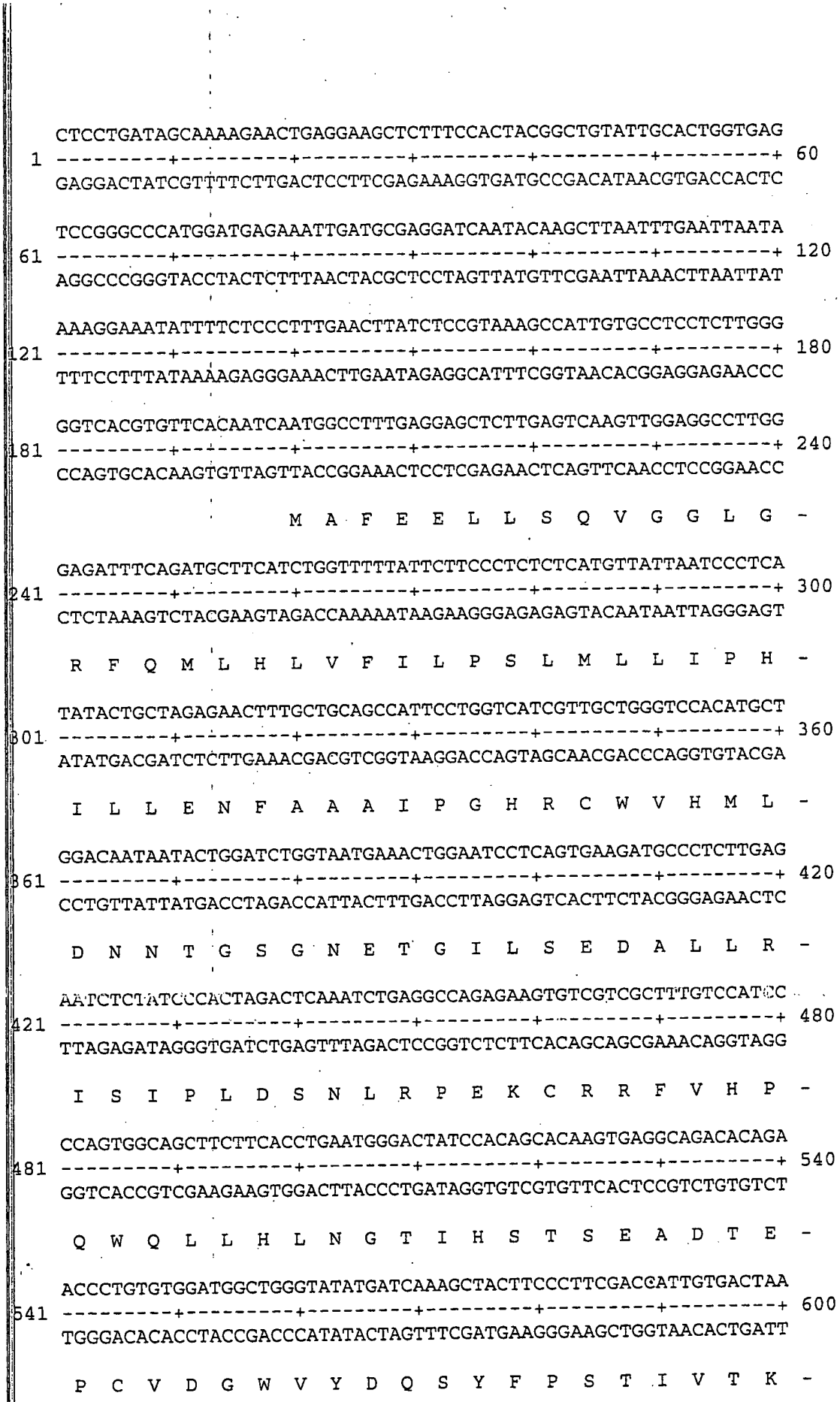


FIGURE 6
Sheet 1 of 5

```
    GTGGGACCTGGTATGTGATTATCAGTCACTGAAATCAGTGGTTCAATTCCTACTTCTGAC
601 ---------+---------+---------+---------+---------+---------+ 660
    CACCCTGGACCATACACTAATAGTCAGTGACTTTAGTCACCAAGTTAAGGATGAAGACTG

     W  D  L  V  C  D  Y  Q  S  L  K  S  V  V  Q  F  L  L  L  T  -

    TGGAATGCTGGTGGGAGGCATCATAGGTGGCCATGTCTCAGACAGGTTTGGGCGAAGATT
661 ---------+---------+---------+---------+---------+---------+ 720
    ACCTTACGACCACCCTCCGTAGTATCCACCGGTACAGAGTCTGTCCAAACCCGCTTCTAA

     G  M  L  V  G  G  I  I  G  G  H  V  S  D  R  F  G  R  R  F  -

    TATTCTCAGATGGTGTTTGCTCCAGCTTGCCATTACTGACACCTGCGCTGCCTTCGCTCC
721 ---------+---------+---------+---------+---------+---------+ 780
    ATAAGAGTCTACCACAAACGAGGTCGAACGGTAATGACTGTGGACGCGACGGAAGCGAGG

     I  L  R  W  C  L  L  Q  L  A  I  T  D  T  C  A  A  F  A  P  -

    CACCTTCCCTGTTTACTGTGTACTACGCTTCTTGGCAGGTTTTTCTTCCATGATCATTAT
781 ---------+---------+---------+---------+---------+---------+ 840
    GTGGAAGGGACAAATGACACATGATGCGAAGAACCGTCCAAAAAGAAGGTACTAGTAATA

     T  F  P  V  Y  C  V  L  R  F  L  A  G  F  S  S  M  I  I  I  -

    ATCAAATAATTCTTTGCCCATTACTGAGTGGATAAGGCCCAACTCTAAAGCCCTGGTAGT
841 ---------+---------+---------+---------+---------+---------+ 900
    TAGTTTATTAAGAAACGGGTAATGACTCACCTATTCCGGGTTGAGATTTCGGGACCATCA

     S  N  N  S  L  P  I  T  E  W  I  R  P  N  S  K  A  L  V  V  -

    AATATTGTCATCTGGTGCCCTTAGTATTGGACAGATAATCCTGGGAGGCTTGGCTTATGT
901 ---------+---------+---------+---------+---------+---------+ 960
    TTATAACAGTAGACCACGGGAATCATAACCTGTCTATTAGGACCCTCCGAACCGAATACA

     I  L  S  S  G  A  L  S  I  G  Q  I  I  L  G  G  L  A  Y  V  -

    CTTCCGAGACTGGCAAACCCTGCACGTGGTGGCGTCAGTACCTTTCCTTGGCCTCCTTCT
961 ---------+---------+---------+---------+---------+---------+ 1020
    GAAGGCTCTGACCGTTTGGGACGTGCACCACCGCAGTCATGGAAAGGAACCGGAGGAAGA

     F  R  D  W  Q  T  L  H  V  V  A  S  V  P  F  L  G  L  L  L  -

    CCTTCAAAGGTGGCTGGTGGAATCTGCTCGGTGGTTGATAATCACCAATAAACTAGATGA
1021 ---------+---------+---------+---------+---------+---------+ 1080
    GGAAGTTTCCACCGACCACCTTAGACGAGCCACCAACTATTAGTGGTTATTTGATCTACT

     L  Q  R  W  L  V  E  S  A  R  W  L  I  I  T  N  K  L  D  E  -

    GGGCTTAAAGGCACTTAGAAAAGTTGCACGCACAAATGGAATAAAGAATGCTGAAGAAAC
1081 ---------+---------+---------+---------+---------+---------+ 1140
    CCCGAATTTCCGTGAATCTTTTCAACGTGCGTGTTTACCTTATTTCTTACGACTTCTTTG

     G  L  K  A  L  R  K  V  A  R  T  N  G  I  K  N  A  E  E  T  -
```

FIGURE 6
Sheet 2 of 5

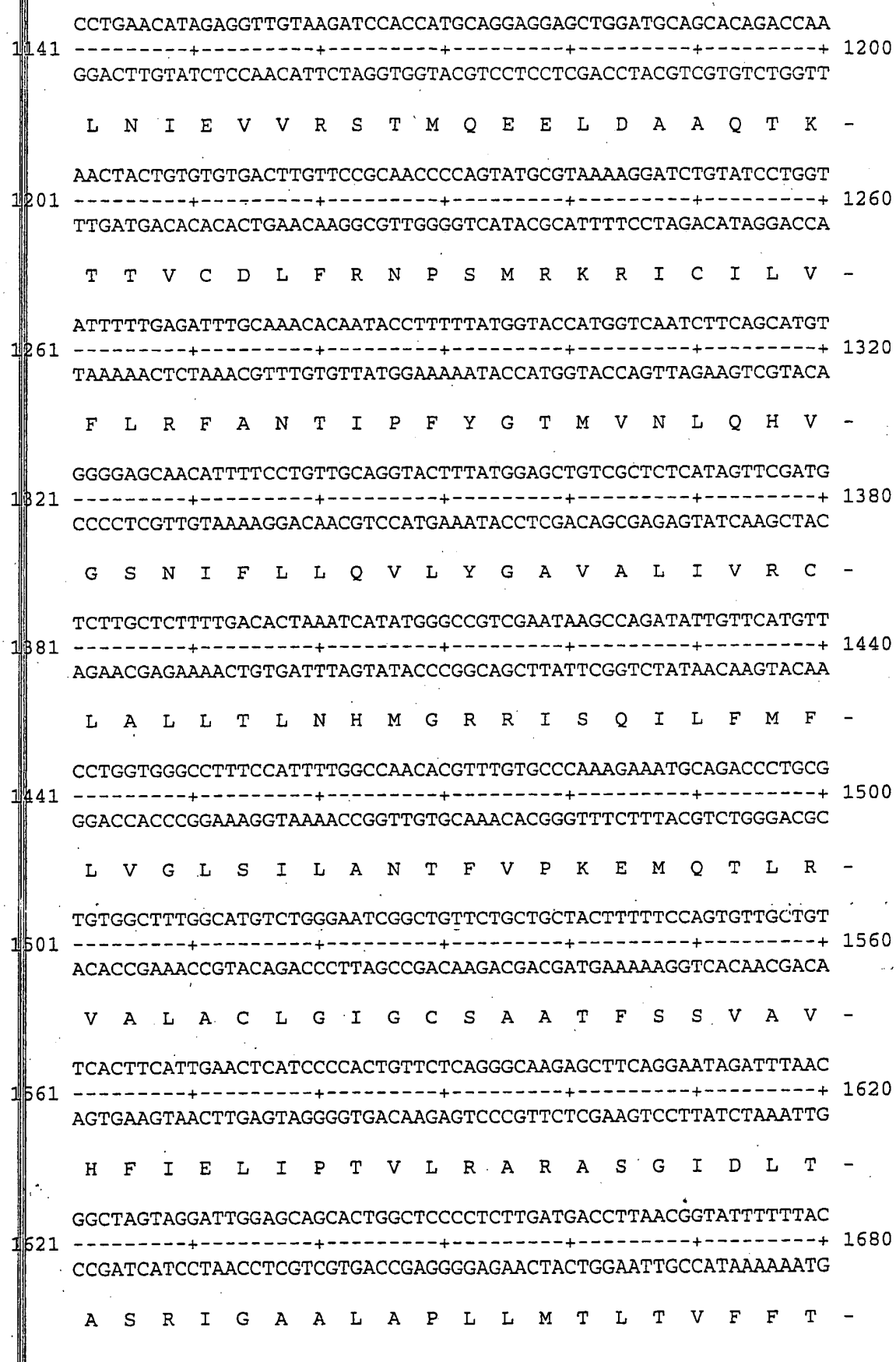


FIGURE 6
Sheet 3 of 5

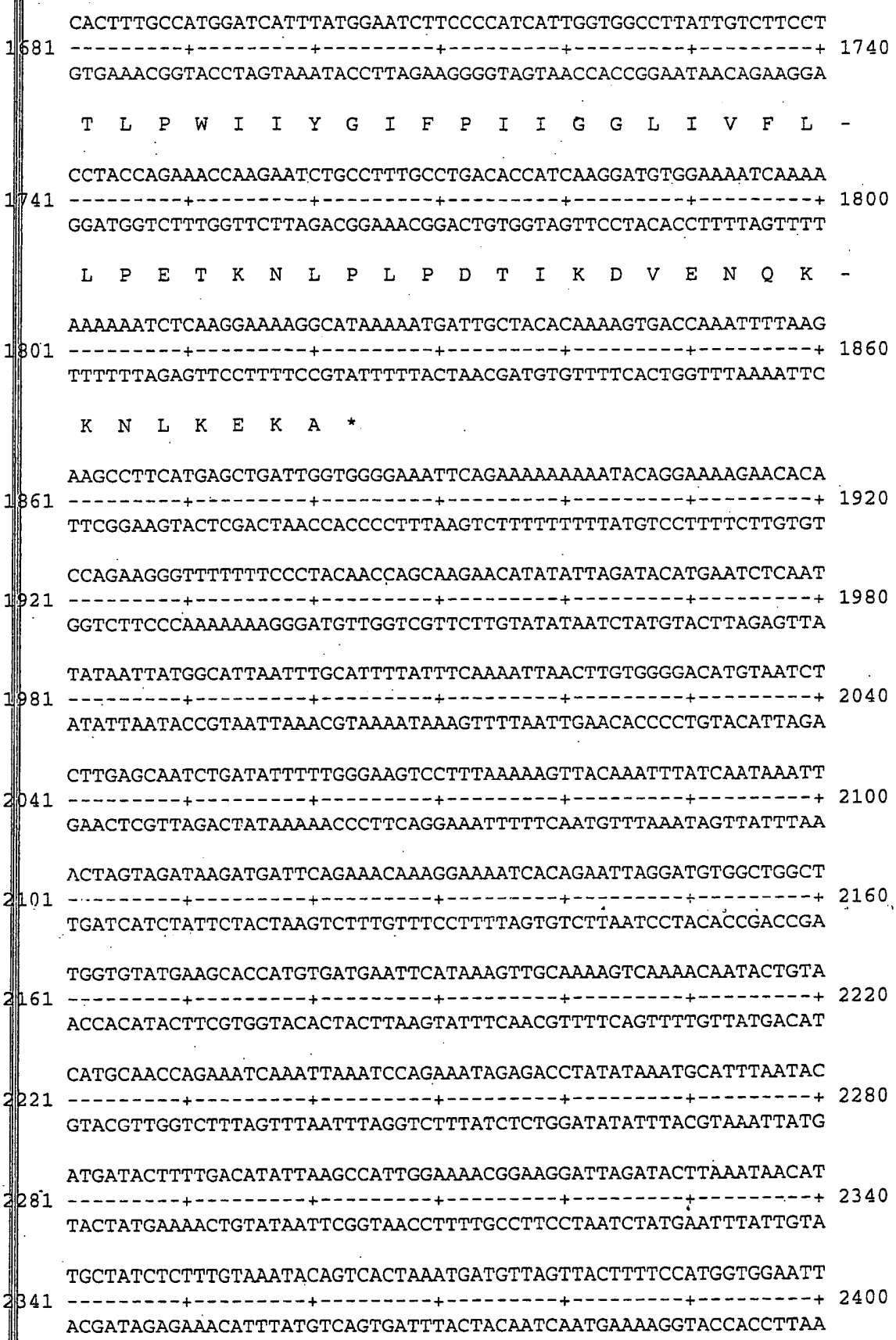


FIGURE 6
Sheet 4 of 5

```
    TTAATTACTTTTTCTTTGTAATTTTTCTCTCTGTATATTTTAAACAAATAGCTGGTATAG
2401 ---------+---------+---------+---------+---------+---------+ 2460
    AATTAATGAAAAAGAAACATTAAAAAGAGAGACATATAAAATTTGTTTATCGACCATATC

    TTTACAATATTATAAAGATATTGTTCAAATTGAAGGGCAAAGGCCAGGTTCAGCAATTTT
2461 ---------+---------+---------+---------+---------+---------+ 2520
    AAATGTTATAATATTTCTATAACAAGTTTAACTTCCCGTTTCCGGTCCAAGTCGTTAAAA

    CAAACTGTATGTACATTTAATAAAATAACTATAAATTAAAAAATTATATTTCAAATGATG
2521 ---------+---------+---------+---------+---------+---------+ 2580
    GTTTGACATACATGTAAATTATTTTATTGATATTTAATTTTTTAATATAAAGTTTACTAC

    TGACTAATAAATGAAAGTACATATAGTAGTAAAGTAATTTCAGGCAAACCTATATAACCA
2581 ---------+---------+---------+---------+---------+---------+ 2640
    ACTGATTATTTACTTTCATGTATATCATCATTTCATTAAAGTCCGTTTGGATATATTGGT

    AAATATAAACTTTCATTTTAAACAGCAAAAAAAAAAAAAAAAAA
2641 ---------+---------+---------+---------+---- 2684
    TTTATATTTGAAAGTAAAATTTGTCGTTTTTTTTTTTTTTTTT
```

FIGURE 6
Sheet 5 of 5

Transport of *p*AH by OAT 1 in HeLa

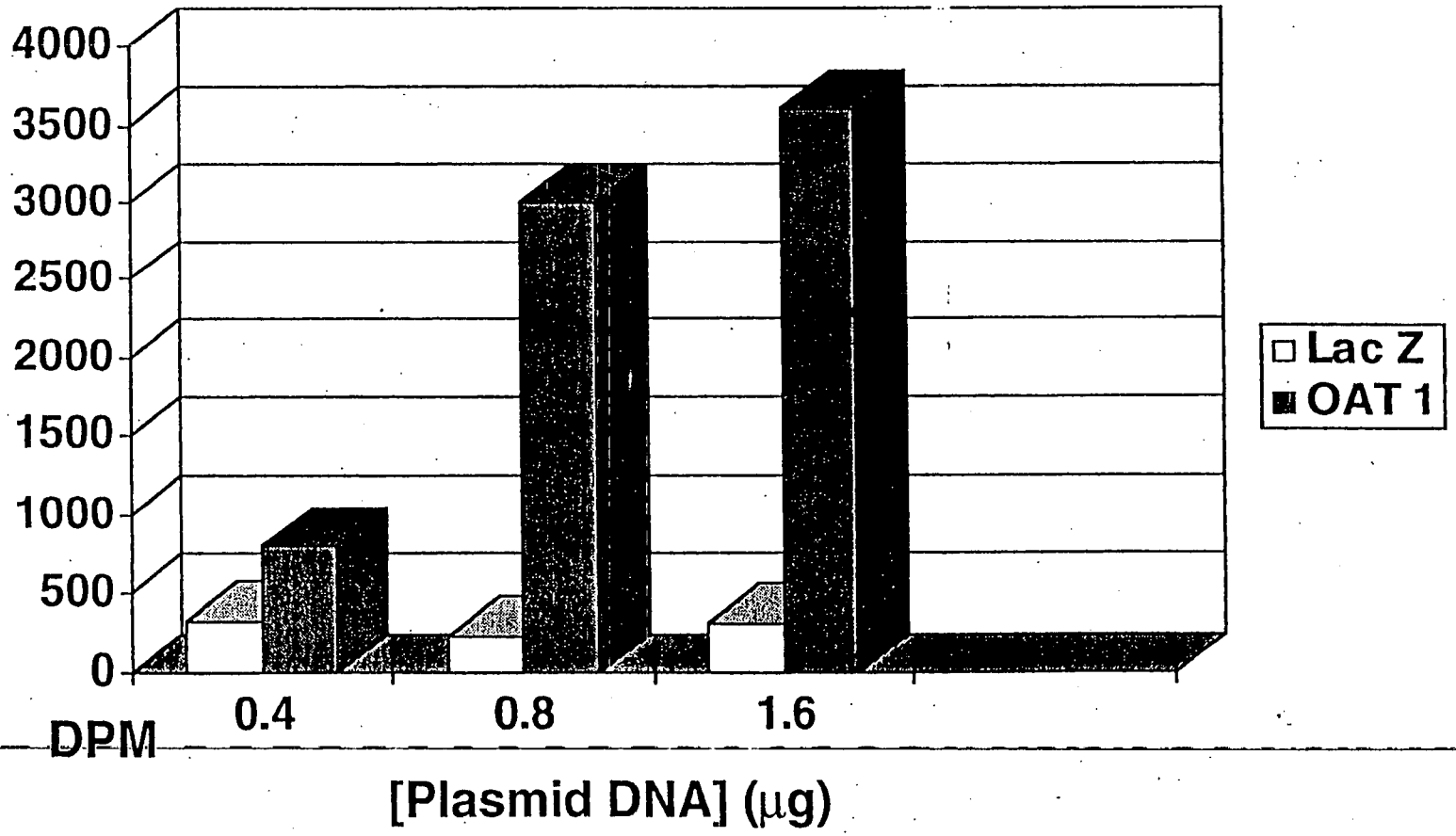


FIGURE 7

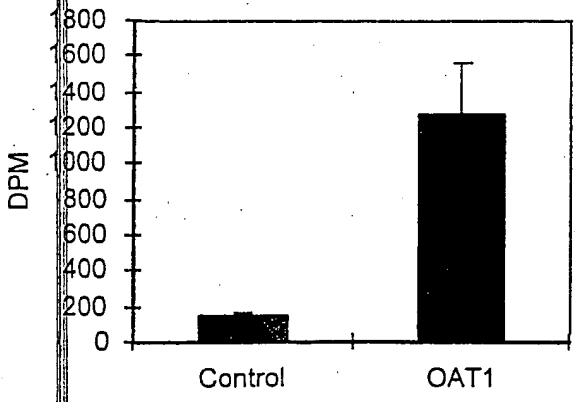


FIGURE 8

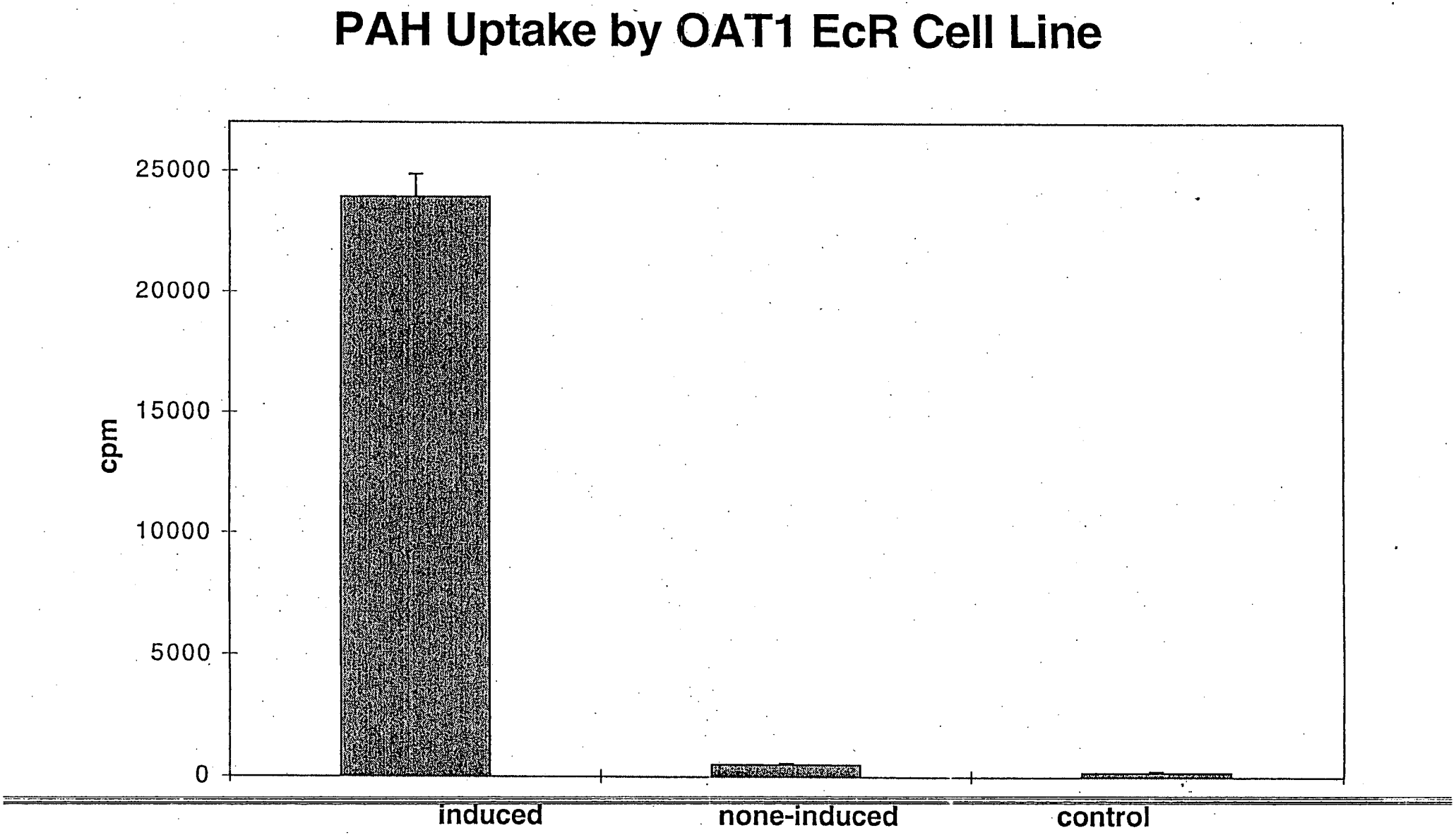

PAH Uptake by OAT1 EcR Cell Line
25000
20000
15000
10000
5000
0
cpm
induced
none-induced
control

FIGURE 9

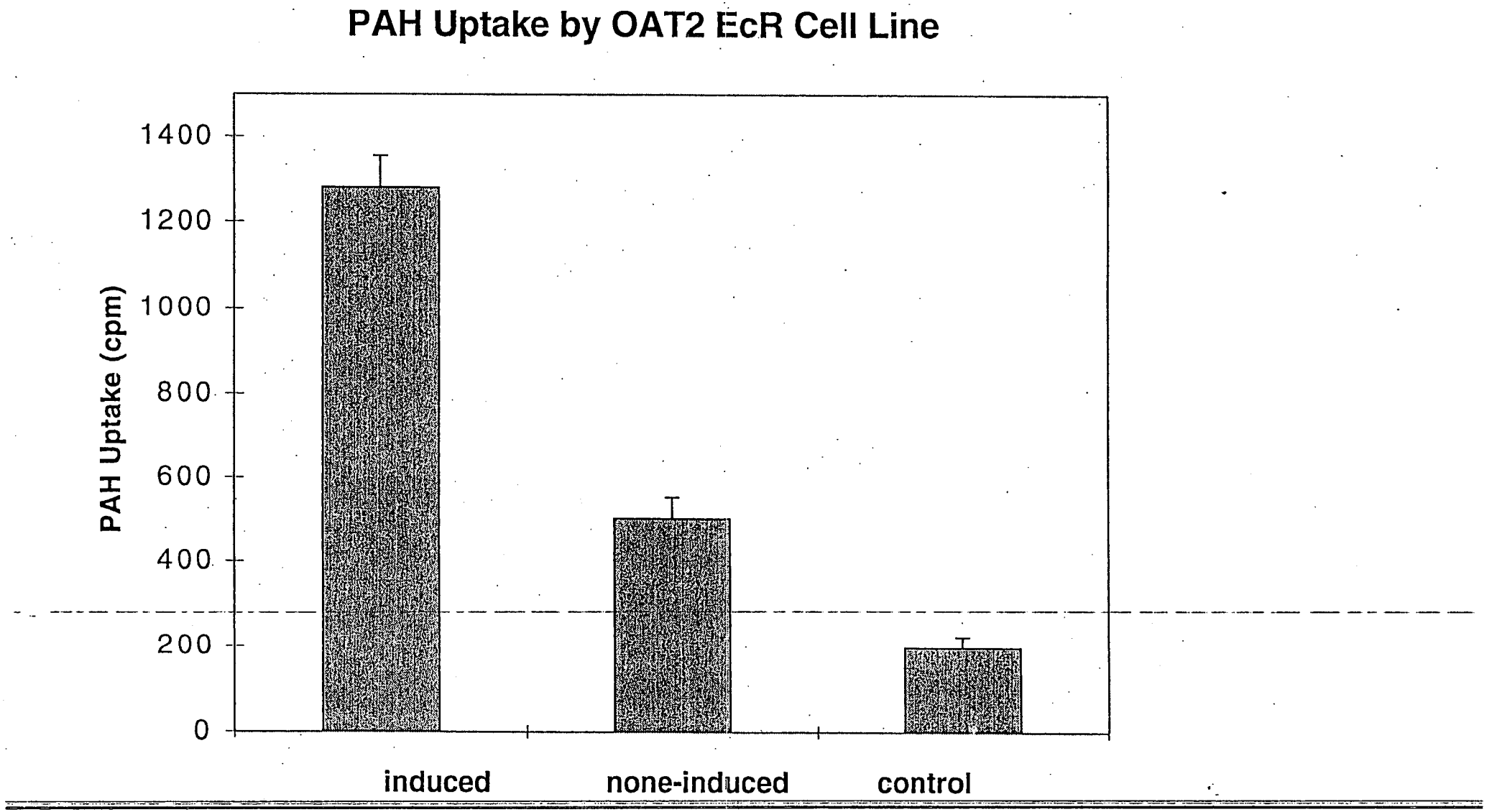

PAH Uptake by OAT2 EcR Cell Line
PAH Uptake (cpm)
1400
1200
1000
800
600
400
200
0
induced
none-induced
control

FIGURE 10

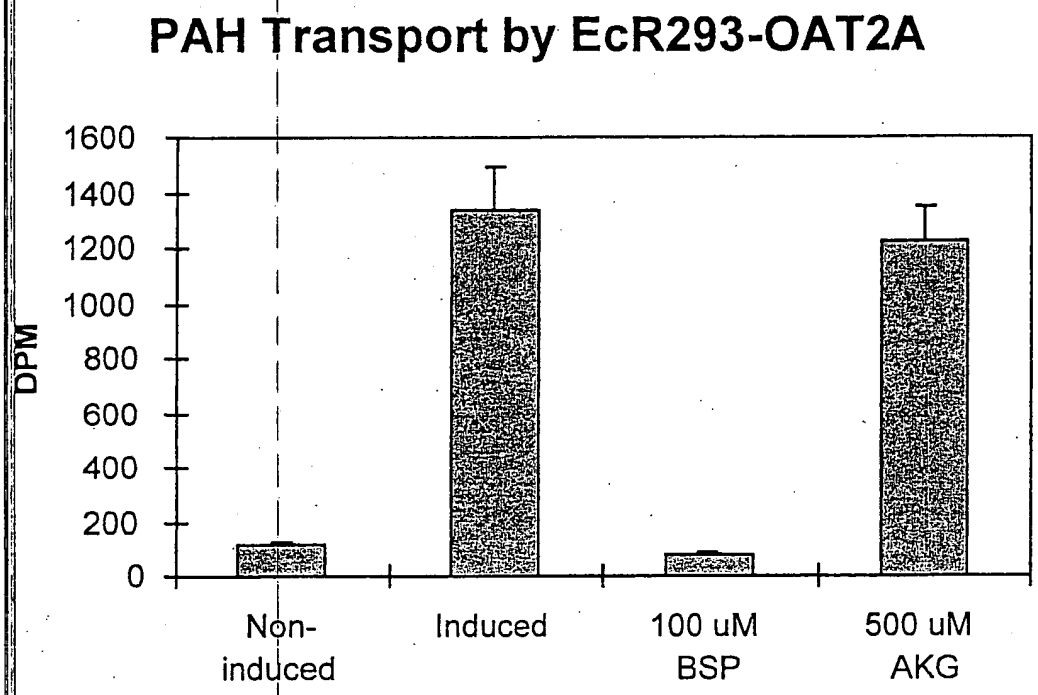

PAH Transport by EcR293-OAT2A
DPM
1600
1400
1200
1000
800
600
400
200
0
Non-induced
Induced
100 uM BSP
500 uM AKG

FIGURE 11

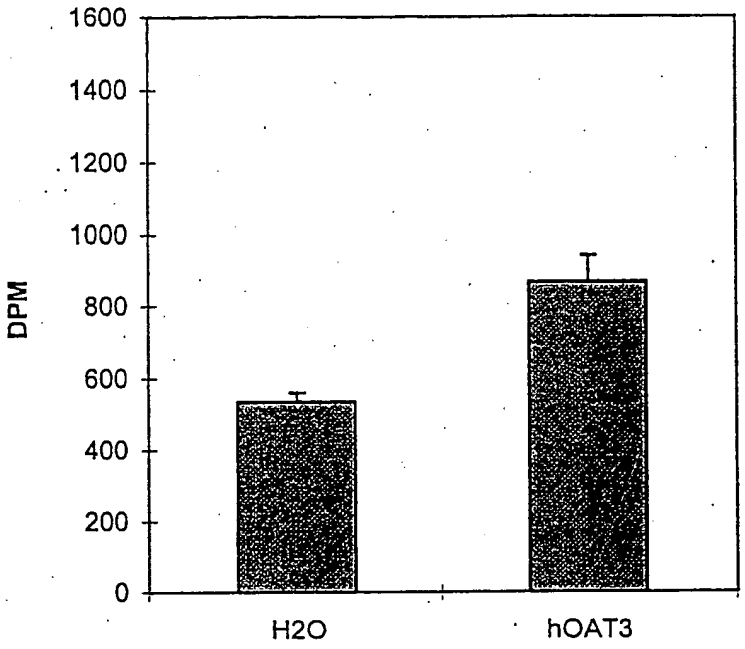
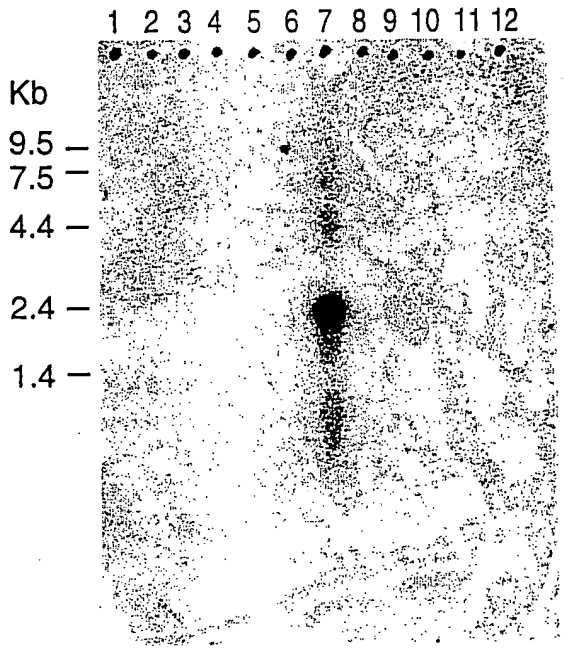
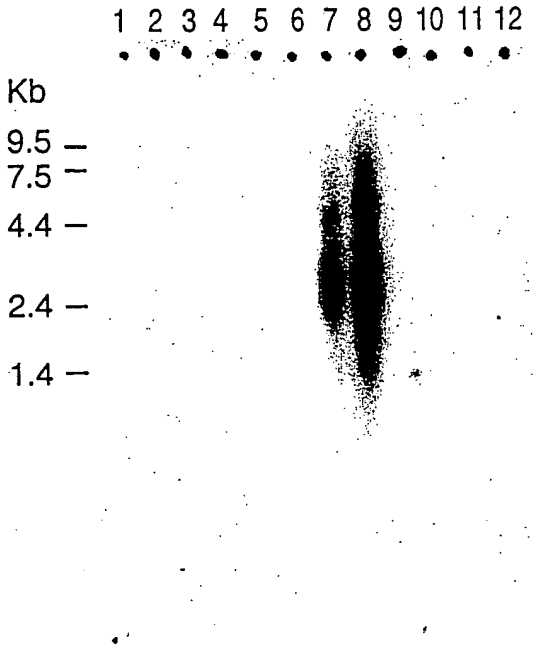


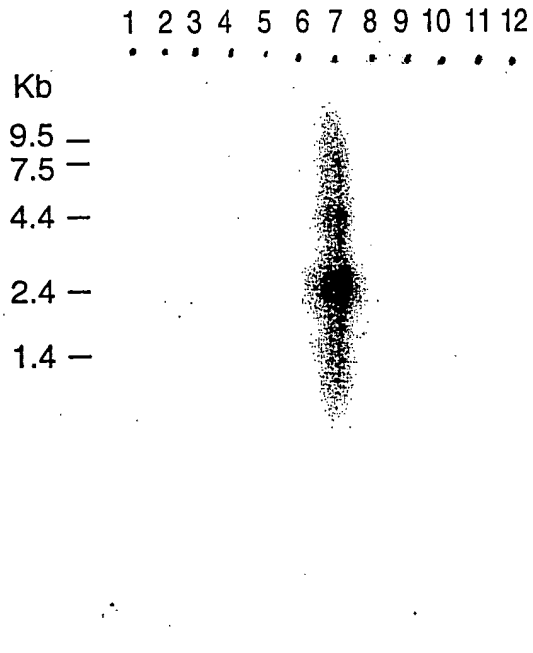
Figure 12: Expression of hOAT3 in Xenopus oocytes. Oocytes were injected with either water or hOAT3 complementary RNA and then assayed for uptake of labeled PAH.



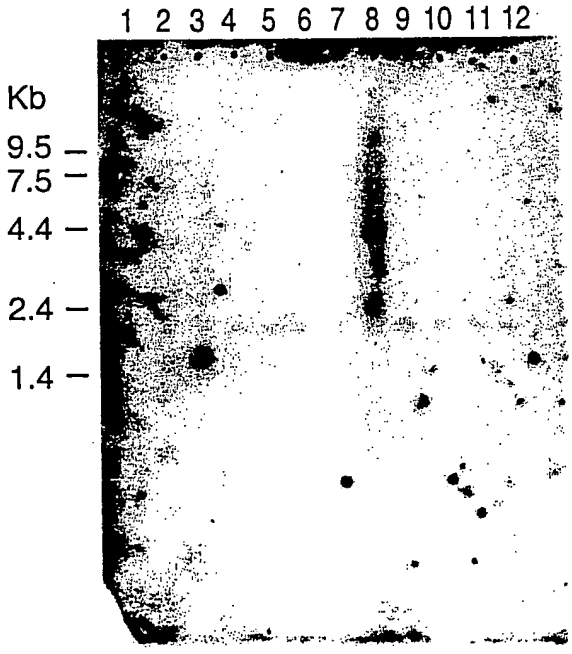
hOAT1



hOAT2



hOAT3



hOAT4

FIGURE 13

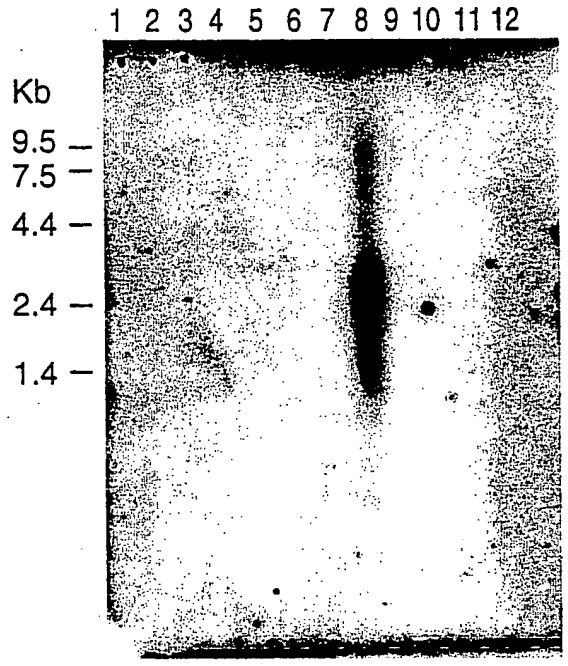


Figure 13: Human Multiple-tissue Northern Blots (Clontech) were hybridized with indicated hOAT cDNAs. Lane numbers corresponds to RNAs extracted from following human tissues:

1. brain
2. heart
3. skeletal muscle
4. colon
5. thymus
6. spleen
7. kidney
8. liver
9. small intestine
10. placenta
11. lung
12. peripheral blood leukocytes.

FIGURE 13

Sheet 2 of 2